

OM protein - protein search, using sw model

Run on: January 28, 2004, 21:07:45 ; Search time 54 Seconds
(without alignments)
1258.055 Million cell updates/sec

Title: US-10-056-884A-2
Perfect score: 2284
Sequence: 1 MALSGNCSRYYPREQSAVP.....DRFPERKHPWQSELLRKYHL 428

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:*

- 1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
- 2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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- 4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
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- 7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
- 8: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
- 9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
- 10: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
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- 12: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
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- 14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
- 15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
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- 18: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
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- 21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
- 22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
- 23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
- 24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	2284	100.0	428	23	AAE28618		Human K+betaM2 pro
2	2271	99.4	428	23	ABB97351		Novel human protei
3	2271	99.4	435	23	ABJ10888		K+beta M6 related
4	1285	56.3	473	24	AAE32081		Human TRICH-15 pro
5	1242	54.4	301	22	ABB11972		Human VM106R.1 hom
6	832	36.4	325	23	ABJ10886		K+beta M6 protein
7	541	23.7	103	23	AAE28628		Human K+betaM2 pro
8	538.5	23.6	228	22	ABB60184		Drosophila melanog
9	538.5	23.6	228	23	ABJ10887		K+beta M6 related
10	367	16.1	101	23	ABJ10893		K+beta M6 related
11	232	10.2	272	22	AAM25877		Human protein sequ
12	231	10.1	290	23	ABP69573		Human polypeptide
13	231	10.1	339	22	AAE10329		Human transporter
14	210.5	9.2	283	21	AAB41802		Human ORFX ORF1566
15	210	9.2	256	20	AAAY34125		Human potassium ch
16	210	9.2	256	23	ABJ10890		K+beta M6 related
17	210	9.2	257	21	AAAY70452		Human membrane cha
18	210	9.2	257	22	AAM40284		Human polypeptide
19	210	9.2	257	23	ABP53971		Human membrane cha
20	210	9.2	257	24	AAG79900		Human MECHP2. Hom
21	210	9.2	287	24	ABR41784		Human DITHP growth
22	210	9.2	302	22	ABG02913		Novel human diagno
23	210	9.2	404	22	AAM42070		Human polypeptide
24	204	8.9	213	22	AAE04898		Human transporter
25	204	8.9	213	23	ABG70920		Human novel membra
26	204	8.9	213	23	ABB78788		Human macroprotein
27	203	8.9	252	23	ABP51311		Human MDDT SEQ ID
28	203	8.9	528	24	AAG79897		Ion channel 47619.
29	202.5	8.9	237	20	AAAY34129		Human potassium ch
30	202.5	8.9	237	22	AAU27754		Human full-length
31	202.5	8.9	237	22	AAM93682		Human polypeptide,
32	202.5	8.9	237	22	AAB95201		Human protein sequ
33	202.5	8.9	237	23	ABP53973		Human beta subunit
34	202.5	8.9	237	23	ABJ10891		K+beta M6 related
35	202.5	8.9	237	23	ABJ10892		K+beta M6 related
36	202.5	8.9	237	23	ABP51811		Human potassium ch
37	201.5	8.8	257	23	ABG70925		Human novel membra
38	201.5	8.8	283	22	AAB95629		Human protein sequ
39	201.5	8.8	283	23	ABG70923		Human novel membra
40	201.5	8.8	283	23	ABG61546		Human transporter
41	193.5	8.5	140	23	ABJ10889		K+beta M6 related
42	193.5	8.5	237	22	AAM93832		Human polypeptide,
43	191	8.4	75	23	ABP34708		Human ORF3681 prot
44	189	8.3	190	22	ABG16368		Novel human diagno
45	189	8.3	205	22	AAM41795		Human polypeptide

ALIGNMENTS

RESULT 1
 AAE28618
 ID AAE28618 standard; Protein; 428 AA.
 XX
 AC AAE28618;
 XX
 DT 27-DEC-2002 (first entry)
 XX
 DE Human K+betaM2 protein.
 XX
 KW Human; potassium channel beta-subunit; K+betaM2 protein; neural disorder;
 KW reproductive disorder; metabolic disorder; premature puberty; nephritis;
 KW endocrine disorder; memory disorder; neuroendocrine condition; asthma;
 KW spermatogenesis; renal disease; learning deficiency; Alzheimer's disease;
 KW neurodegenerative disease; proliferative disorder; autoimmune disease;
 KW carcinoid tumour; blood coagulation disease; blood platelet disease;
 KW rheumatoid arthritis; allergy; hyperproliferative disease; gene therapy;
 KW graft-versus-host disease; organ rejection; antisterility; thrombolytic;
 KW antiinflammatory; neuroprotective; anti-Parkinsonian; immunosuppressive;
 KW nephrotropic; cytostatic; nootropic; hypotensive; vulnerary.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 25..127
 FT /label= Potassium_channel_tetramerisation_domain
 FT Domain 243..263
 FT /label= Transmembrane_domain
 XX
 PN WO200266601-A2.
 XX
 PD 29-AUG-2002.
 XX
 PF 24-JAN-2002; 2002WO-US02332.
 XX
 PR 24-JAN-2001; 2001US-263872P.
 PR 14-FEB-2001; 2001US-269794P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Feder J, Lee L, Chen J, Jackson D, Ramanathan C, Siemers N;
 PI Chang H, Carroll P;
 XX
 DR WPI; 2002-691617/74.
 DR N-PSDB; AAD46068.
 XX
 PT New potassium channel beta-subunit, K+betaM2, proteins and nucleic
 PT acids, useful for diagnosing, treating and/or preventing e.g.
 PT reproductive, neural, metabolic, endocrine, memory, neurodegenerative
 PT disorders or diseases -
 XX
 PS Claim 5; Page 347-349; 366pp; English.
 XX
 CC The present invention relates to human potassium channel beta-subunit
 CC (K+betaM2) proteins and polynucleotides encoding such proteins. The
 CC K+betaM2 sequences are useful for diagnosing, treating and/or preventing
 CC reproductive disorders, neural disorders, disorders related to aberrant

CC potassium regulation or hyper potassium channel activity, metabolic
 CC disorders (e.g. premature puberty), endocrine disorders (e.g. aberrant
 CC growth hormone synthesis and/or secretion), memory disorder, disorders
 CC of the testis (e.g. spermatogenesis), neuroendocrine condition related
 CC to aberrant thyroid hormone release, renal disease or disorders (e.g.
 CC nephritis), disorders related to aberrant higher brain function (e.g.
 CC learning deficiencies), neurodegenerative diseases (e.g. Alzheimer's
 CC disease), proliferative disorders (e.g. carcinoid tumour) and disorders
 CC involving excessive smooth muscle tone or excitability (e.g. asthma).
 CC They may be used to modulate haemostatic or thrombolytic activity, to
 CC treat or prevent blood coagulation diseases or disorders, blood platelet
 CC diseases, wounds, autoimmune diseases, disorders or conditions (e.g.
 CC rheumatoid arthritis), allergic reactions (e.g. asthma), organ rejection
 CC or graft-versus-host disease, and hyperproliferative diseases. K+betaM2
 CC sequences are also used in gene therapy. The present sequence is human
 CC K+betaM2 protein.

XX

SQ Sequence 428 AA;

Query Match 100.0%; Score 2284; DB 23; Length 428;
 Best Local Similarity 100.0%; Pred. No. 1.9e-220;
 Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MALSGNCSRYYPREQGSAVPNSFPEVVVLNVGGQVYFTRHSTLISIPHSLLWKMFSPKRD	60
Db	1	MALSGNCSRYYPREQGSAVPNSFPEVVVLNVGGQVYFTRHSTLISIPHSLLWKMFSPKRD	60
Qy	61	TANDLAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLDPHFPEKGRLKREAEYFQLPDLVK	120
Db	61	TANDLAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLDPHFPEKGRLKREAEYFQLPDLVK	120
Qy	121	LLTPDEIKQSPDEFCHSDFEDASQGS DTRICPPSSLLPADRKWGFITVGYRG SCTLGREG	180
Db	121	LLTPDEIKQSPDEFCHSDFEDASQGS DTRICPPSSLLPADRKWGFITVGYRG SCTLGREG	180
Qy	181	QADAKFRRVPRIILVCGRISLAKEVFGETL NESRDPDRAPERYTSRFY LKFKHLERAFDML	240
Db	181	QADAKFRRVPRIILVCGRISLAKEVFGETL NESRDPDRAPERYTSRFY LKFKHLERAFDML	240
Qy	241	SECGFHMVACNSSVTASF INQYTD D KIWSSY TEYVFYREPSRWSPSHCDCCCKNGKGDKE	300
Db	241	SECGFHMVACNSSVTASF INQYTD D KIWSSY TEYVFYREPSRWSPSHCDCCCKNGKGDKE	300
Qy	301	GESGTSCNDLSTSSCDSQSEASSPQETVICGPVTRQTNIQT LDRPIKKG PVQLIQQSEMR	360
Db	301	GESGTSCNDLSTSSCDSQSEASSPQETVICGPVTRQTNIQT LDRPIKKG PVQLIQQSEMR	360
Qy	361	RKSDLLRILTSGSRESNMSSKKKAVKEKLSIEEELEKCIQDFLKKKIPDRFPERKHPWQS	420
Db	361	RKSDLLRILTSGSRESNMSSKKKAVKEKLSIEEELEKCIQDFLKKKIPDRFPERKHPWQS	420
Qy	421	ELLRKYHL	428
Db	421	ELLRKYHL	428

RESULT 2

ABB97351

ID ABB97351 standard; Protein; 428 AA.

XX

AC ABB97351;

XX

DT 27-JUN-2002 (first entry)

XX

DE Novel human protein SEQ ID NO: 619.

XX

KW Human; antianaemic; vulnerary; antiinflammatory; immunomodulator;

KW antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy;

KW neuroprotective; antiparkinsonian; protein therapy; EST;

KW expressed sequence tag.

XX

OS Homo sapiens.

XX

PN WO200222660-A2.

XX

PD 21-MAR-2002.

XX

PF 10-SEP-2001; 2001WO-US26015.

XX

PR 11-SEP-2000; 2000US-0659671.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;

PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;

XX

DR WPI; 2002-292408/33.

DR N-PSDB; ABN32537.

XX

PT An isolated polynucleotide for treating diseases associated with its

PT encoded polypeptide such as cancer and multiple sclerosis -

XX

PS Example 2; SEQ ID NO 619; 509pp; English.

XX

CC The present invention provides the protein and coding sequences of 444

CC novel human proteins. These were isolated from expressed sequences tags

CC (ESTs). They can be used to stimulate cell growth, to regulate

CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth

CC e.g. in burn treatment, to regulate the immune system e.g. to treat

CC multiple sclerosis, to regulate activin or inhibin e.g. to treat

CC infertility, to regulate haemostasis or thrombolysis e.g. to treat

CC stroke and cancer, to screen for drugs, to treat inflammatory conditions

CC e.g. rheumatoid arthritis, and to treat nervous system disorders e.g.

CC Parkinson's disease. The present sequence is a protein of the invention.

XX

SQ Sequence 428 AA;

Query Match 99.4%; Score 2271; DB 23; Length 428;

Best Local Similarity 99.5%; Pred. No. 3.8e-219;

Matches 426; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MALSGNCSRYYPREQGSAPVNSFPVVVELNVGGQVYFTRHSTLISIPHSLWKMFSKRD 60

|||||

Db 1 MALSGNCSRYYPREQGSAPVNSFPVVVELNVGGQVYFTRHSTLISIPHSLWKMFSKRD 60

Qy	61	TANDLAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLDPHFPEKGRLKREAEYFQLPDLVK	120
Db	61	TANDLAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLDPHFPEKGRLKREAEYFQLPDLVK	120
Qy	121	LLTPDEIKQSPDEFCHSDFEDASQGS DTRICPPSSLLPADRKWGFITVGYRG SCTLGREG	180
Db	121	LLTPDEIKQSPDEFCHSDFEDASQGS DTRICPPSSLLPADRKWGFITVGYRG SCTLGREG	180
Qy	181	QADAKFRRVPRILVCGRISLAKEVFGETL NESRDPDRAPER YTSRFYLKFKHLERA F DML	240
Db	181	QADAKFRRVPRILVCGRISLAKEVFGETL NESRDPDRAPER YTSRFYLKFKHLERA F DML	240
Qy	241	SECGFHMVACNSSVTASFINQYTDDKI WSSYTEYVFYREPSRWSPSHDC CCKNGKGDKE	300
Db	241	SECGFHMVACNSSVTASFINQYTDDKI WSSYTEYVFYREPSRWSPSHDC CCKNGKGDKE	300
Qy	301	GESGTSCNDLSTSSCDSQSEASSPQETVICGPVTRQTNIQTLDRPIKKG PVQLIQQSEMR	360
Db	301	GESGTSCNDLSTSSCDSQSEASSPQETVICGPVTRQTNIQTLDRPIKKG PVQLIQQSEMR	360
Qy	361	RKSDLLRIITSGSRESNMSSKKKAVKEKLSIEEELEKCIQDFLKKKIPDRFPERKHPWQS	420
Db	361	RKSDLLRIITSGSRESNMSSKKKAVKEKLSIEEELEKCIQDFLKKKIPDRFPERKHPWQS	420
Qy	421	ELLRKYHL	428
Db	421	ELLRKYHL	428

RESULT 3

ABJ10888

ID ABJ10888 standard; Protein; 435 AA.

XX

AC ABJ10888;

XX

DT 05-DEC-2002 (first entry)

XX

DE K+beta M6 related protein SEQ ID No 4.

XX

KW Cytostatic; cardiant; neuroprotective; immunomodulator; antimigraine;
 KW sedative; gynaecological;; potassium channel beta subunit; K+betaM6;
 KW gastrointestinal; reproductive; neural; sleep; low DNA repair capacity;
 KW hyperpotassium channel activity; cardiovascular; melatonin synthesis;
 KW mammary cancer tumorigenesis; pineal gland associated disorder;
 KW pulmonary disorder; immune disorder; NF-kB activity; migraine headache;
 KW low free-radical buffering capacity; delayed sleep phase syndrome;
 KW circadian cycle; melatonin secretion; cancer.

XX

OS Homo sapiens.

XX

PN WO200270727-A2.

XX

PD 12-SEP-2002.

XX

PF 21-FEB-2002; 2002WO-US05674.

XX

PR 27-MAR-2001; 2001US-278953P.

XX

PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX

PI Feder J, Lee L, Chen J, Jackson DG, Ramanathan C, Siemers N;
PI Chang H;

XX

DR WPI; 2002-713455/77.

XX

PT New polynucleotide encoding human potassium channel beta subunit
PT polypeptide, useful for diagnosing, preventing, treating or
PT ameliorating e.g. cancer -

XX

PS Disclosure; Fig 2; 332pp; English.

XX

The invention relates to an isolated polynucleotide encoding a potassium channel beta subunit (K+betaM6) polypeptide or its variants. The human potassium beta subunit polynucleotide or polypeptide is useful for diagnosing, preventing, treating or ameliorating a pathological condition such as gastrointestinal, reproductive, neural, sleep, cardiovascular or pulmonary disorders, a disorder related to hyperpotassium channel activity, an immune disorder related to aberrant NF-kB activity, pineal gland associated disorders, migraine headaches, disorders associated with aberrant melatonin synthesis and/or release or with low DNA repair capacities or low free-radical buffering capacity, delayed sleep phase syndrome, aberrations in circadian cycle, mammary cancer tumourigenesis, age related disorders associated with decreased melatonin secretion, or cancer. This sequence represents a potassium channel beta subunit (K+betaM6) related protein of the invention.

XX

SQ Sequence 435 AA;

Query Match 99.4%; Score 2271; DB 23; Length 435;
Best Local Similarity 99.5%; Pred. No. 3.9e-219;
Matches 426; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	MALSGNCSRYYPREQGSAVPNSFPEVVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRD	60
Db	8	MALSGNCSRYYPREQGSAVPNSFPEVVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRD	67
Qy	61	TANDLAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLDPDHFPEKGRLKREAEYFQLPDLVK	120
Db	68	TANDLAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLDPDHFPEKGRLKREAEYFQLPDLVK	127
Qy	121	LLTPDEIKQSPDEFCHSDFEDASQGS DTRICPPSSLLPADRKWGFITVGYRG SCTLGREG	180
Db	128	LLTPDEIKQSPDEFCHSDFEDASQGS DTRICPPSSLLPADRKWGFITVGYRG SCTLGREG	187
Qy	181	QADAKFRRVPRIILVCGRISLAKEVFGETL NESRDPDRAPERYTSRFYLKFKHLERAFDML	240
Db	188	QADAKFRRVPRIILVCGRISLAKEVFGETL NESRDPDRAPERYTSRFYLKFKHLERAFDML	247
Qy	241	SECGFH MVACNSSVTASFINQYTDDKIWSSY TEYVFYREPSRWSPSHCDCCCKNGKGDKE	300
Db	248	SECGFH MVACNSSVTASFINOYTDDKIWSSY TEYVFYREPSRWSPSHCDCCCKNGKGDKE	307

Qy 301 GESGTSCNDLSTSSCDSQSEASSPQETVICGPVTRQTNIQTLDLRPIKKGPVQLIQQSEMR 360
 |||||
 Db 308 GESGTSCNDLSTSSCDSQSEASSPQETVICGPVTRQTNIQTLDLRPIKKGPVQLIQQSEMR 367

Qy 361 RKSDLLRIITSGSRESNMSSKKKAVKEKLSIEEELEKCIQDFLKKKIPDRFPERKHPWQS 420
 |||||
 Db 368 RKSDLLRLTITSGSRESNMSSKKKAVKEKLSIEEELEKCIQDFLKIKIPDRFPERKHPWQS 427

Qy 421 ELLRKYHL 428
 |||||
 Db 428 ELLRKYHL 435

RESULT 4

AAE32081

ID AAE32081 standard; Protein; 473 AA.

XX

AC AAE32081;

XX

DT 24-MAR-2003 (first entry)

XX

DE Human TRICH-15 protein.

XX

KW Human; transporter and ion channel; TRICH; atherosclerosis; cancer;
 KW gene therapy.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1..39

FT /label= Signal_peptide

FT Protein 40..473

FT /note= "Mature human TRICH protein"

FT Domain 44..151

FT /note= "K+ channel tetramerisation domain"

XX

PN WO200283712-A2.

XX

PD 24-OCT-2002.

XX

PF 12-APR-2002; 2002WO-US11760.

XX

PR 12-APR-2001; 2001US-283440P.

PR 20-APR-2001; 2001US-285592P.

PR 27-APR-2001; 2001US-287263P.

PR 04-MAY-2001; 2001US-288666P.

PR 18-MAY-2001; 2001US-292042P.

PR 25-MAY-2001; 2001US-293724P.

PR 22-JAN-2002; 2002US-351107P.

XX

PA (INCY-) INCYTE GENOMICS INC.

XX

PI Baughn MR, Elliott VS, Hafalia AJA, Yang J, Walia NK, Ramkumar J;
 PI Forsythe IJ, Lu Y, Tang YT, Yue H, Raumann BE, Lal PG, Azimzai Y;
 PI Lu DAM, Gandhi AR, Thornton M, Nguyen DB, Arvizu CS, Emerling BM;
 PI Swarnakar A, Yao MG, Ding L, He A, Griffin JA, Sanjanwala MM;
 PI Gietzen KJ, Lee EA, Xu Y, Au-Young JK, Das D, Lee SY, Chang H;

XX
DR WPI; 2003-092996/08.
DR N-PSDB; AAD49513.

XX
PT New human functional transporters and ion channels (TRICH)
PT polypeptides, useful for preparing a composition for diagnosing or
PT treating a disease associated with decreased expression or
PT overexpression of TRICH e.g. cancer -

XX
PS Claim 1; Page 177-178; 204pp; English.

XX
CC The invention relates to human transporters and ion channels (TRICH)
CC polypeptides and nucleic acid molecules encoding such polypeptides.
CC TRICH proteins are useful for preparing compositions for diagnosing or
CC treating diseases or conditions associated with decreased expression
CC or overexpression of functional TRICH e.g. atherosclerosis or cancer.
CC The invention is useful in gene therapy. The present sequence is
CC human TRICH protein.

XX
SQ Sequence 473 AA;

Query Match 56.3%; Score 1285; DB 24; Length 473;
Best Local Similarity 60.8%; Pred. No. 6e-120;
Matches 268; Conservative 47; Mismatches 96; Indels 30; Gaps 9;

Qy 16 GSAVENSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFS PKRDTA-----NDLAKDSK 70
| : : ||||| :|||:| : | ||| :| :||:
Db 35 GPCAPSPFPEVVELNVGGQVYVTKHSTLLSVPDSTLASMFS PSSPRGGARRRGELPRDSR 94

Qy 71 GRFFIDRDGFLFRYILDYLRDRQVLPDHFPEKGRLKREAIFYQLPDLVKLLTPDEIKQS 130
|||::||::|: ||:|||| || ||||| ||||::| ||:
Db 95 ARFFIDRDGFLFRYVLDYLRDKQLALPEHFPEKERLLREAIFYQLTDLVKLLSPKVTKON 154

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Qy      131 P--DEFCHSDFED-ASQGS DTRIC--PPSLLPA-----DRKWGFITVGYR 171
          || | || || ||| :      :: :::      :: ||::|:|
Db      155 SLNDEGCOSDLEDNVSOGSSDALLLRGAAA VPSGPGA HGGGGGGGAODKRS GFLT LGYR 214

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QY 172 GSCTLGREGQADAKFRRVPRILVCGRISLAKEVFGETLNESRDPDRAPERYSRFYLKFK 231
||| |:||||||| ||:||||:||||||:||||||| ||:|||||||
Db 215 GSYTTVRDNOADAKFRRVARIMVCGRIALAKEVFGDTLNESRDPDROPEKYTSRFYLKFT 274

Qy 232 HLERAFDMLSECGFHMVACNSSVTASFINQYTDDKIWSSYTEYVFYREPSR-WSPSHCDC 290
::||| ||| ||||||||| |:|:|| | ||||| :|:| | : ||
Db 275 YLEOAFDRLSEAGFHMVACNSSGTAAFVNQYRDDKIWSSYTEYIFFRPPOKIVSPKQEHE 334

QY 291 CCKNGK-GDKEGESGTSCNDLSTSSCDSQSEASSPQETVICG--PVTRQTNIQTLDRIPIK 347
|:| || |||||:||||||| |||:|:| | ||||| |
Db 335 DRKHDKVTDKGESGTSCNELSTSSCDSHSEASTPDNPSSAQOATAHQPNLTLTLDPRSK 394

Qy	348	KGPVQLIQQSEMRKSDLLRLITSGSRESNMSSKKKAVKEKLSIEEELEKCIQDFLKKKI	407
		: : : :	
Db	395	KAPVQWIPPPDKRRNSELFOTLISKSRETNLSKKK--VCEKLSVEEEMKKCIQDFKKIHI	452

Qy 408 PDRFPERKHPWQSELLRKYHL 428
|| ||||| |||||:|| |
Db 453 PDYFPERKROWQSELLQKYGL 473

RESULT 5

ABB11972

ID ABB11972 standard; peptide; 301 AA.

XX

AC ABB11972;

XX

DT 11-JAN-2002 (first entry)

XX

DE Human VM106R.1 homologue, SEQ ID NO:2342.

XX

KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnerary; antiulcer.

XX

OS Homo sapiens.

XX

PN WO200157188-A2.

XX

PD 09-AUG-2001.

XX

PF 05-FEB-2001; 2001WO-US03800.

XX

PR 03-FEB-2000; 2000US-0496914.

PR 27-APR-2000; 2000US-0560875.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Tang YT, Liu C, Drmanac RT;

XX

DR WPI; 2001-457740/49.

DR N-PSDB; ABA09216.

XX

PT Human proteins and DNA encoding sequences useful for preventing,
PT treating or ameliorating a medical condition in a mammalian subject
PT e.g. arthritis and cancer -

XX

PS Claim 20; Page 289; 1963pp; English.

XX

CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC invention also relates to vectors and recombinant host cells comprising a
CC nucleotide of the invention, methods of producing the novel polypeptides,
CC antibodies against the polypeptides, methods of detecting the nucleotides
CC or polypeptides in a sample, and methods of identifying compounds which
CC bind to polypeptides of the invention. Although novel, many of the
CC polypeptides of the invention have homology to known proteins, thereby

AC ABJ10886;
 XX
 DT 05-DEC-2002 (first entry)
 XX
 DE K+beta M6 protein SEQ ID No 2.
 XX
 KW Cytostatic; cardiant; neuroprotective; immunomodulator; antimigraine;
 KW sedative; gynaecological;; potassium channel beta subunit; K+betaM6;
 KW gastrointestinal; reproductive; neural; sleep; low DNA repair capacity;
 KW hyperpotassium channel activity; cardiovascular; melatonin synthesis;
 KW mammary cancer tumourigenesis; pineal gland associated disorder;
 KW pulmonary disorder; immune disorder; NF-kB activity; migraine headache;
 KW low free-radical buffering capacity; delayed sleep phase syndrome;
 KW circadian cycle; melatonin secretion; cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200270727-A2.
 XX
 PD 12-SEP-2002.
 XX
 PF 21-FEB-2002; 2002WO-US05674.
 XX
 PR 21-FEB-2001; 2001US-270132P.
 PR 27-MAR-2001; 2001US-278953P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Feder J, Lee L, Chen J, Jackson DG, Ramanathan C, Siemers N;
 PI Chang H;
 XX
 DR WPI; 2002-713455/77.
 DR N-PSDB; ABT09812.
 XX
 PT New polynucleotide encoding human potassium channel beta subunit
 PT polypeptide, useful for diagnosing, preventing, treating or
 PT ameliorating e.g. cancer -
 XX
 PS Claim 5; Fig 1; 332pp; English.
 XX
 CC The invention relates to an isolated polynucleotide encoding a potassium
 CC channel beta subunit (K+betaM6) polypeptide or its variants. The human
 CC potassium beta subunit polynucleotide or polypeptide is useful for
 CC diagnosing, preventing, treating or ameliorating a pathological condition
 CC such as gastrointestinal, reproductive, neural, sleep, cardiovascular or
 CC pulmonary disorders, a disorder related to hyperpotassium channel
 CC activity, an immune disorder related to aberrant NF-kB activity, pineal
 CC gland associated disorders, migraine headaches, disorders associated with
 CC aberrant melatonin synthesis and/or release or with low DNA repair
 CC capacities or low free-radical buffering capacity, delayed sleep phase
 CC syndrome, aberrations in circadian cycle, mammary cancer tumourigenesis,
 CC age related disorders associated with decreased melatonin secretion, or
 CC cancer. This sequence represents the potassium channel beta subunit
 CC (K+betaM6) protein of the invention.
 XX
 SQ Sequence 325 AA;

Query Match 36.4%; Score 832; DB 23; Length 325;
 Best Local Similarity 54.0%; Pred. No. 1.2e-74;
 Matches 170; Conservative 41; Mismatches 56; Indels 48; Gaps 6;

```

Qy      4 SGNCSRYYPREQGSAVPNSFPEVVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTAN 63
      ||: |      || |  ||::||| || |  ||:|:|  |||:|:  ::
Db      20 SGSSS-----SSAEPPLFPDIVELNVGGQVYVTRRCTVVSVPDSLLWRMFTQQQ--PQ 70

Qy      64 DLAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLDPHFPEKGRLKREAEYFQLPDLVKLL- 122
      :||:|||||:||||| ||| ||:||||:|: ||:|||||:|:|: |
Db      71 ELARDSKGRFFLDRDGFLFRYILDYLRDLQLVLPDYFPERSRLEREAEYFELPELVRRLG 130

Qy      123 TPDEIKQSP-----DEFCHSDFEDASQ-----GS 146
      | : |      || : : |      |:
Db      131 APQQPGPGPPPSRRGVHKEGSLGDELLPLGYSEPEQQEGASAGAPSPTLELASRSPSGGA 190

Qy      147 DTRICPPSSLLPADRKWGFITVGYRGSCITLGREGQADAKFRRVPRIILVCGRISLAKEVFG 206
      : || |  |: |:|:| || |:|: ||| || | |||: ||| |||
Db      191 AGPLLTQSQSLDGSRRSGYITIGYRGSYTIGRDAQADAKFRRVARITVCGKTSLAKEVFG 250

Qy      207 ETLNESRDPDRAPERYTSRYLKFHKLERAFLMLSECGFHMVACNSSVTASFIN--QYTD 264
      :||||| ||| |||:| ||| ||: || ||| |||:|: | :| : :
Db      251 DTLNESRDPDRPPERYSRYLKFNFLEQAFDKLSESGFHMVACSSSTGTCAFASSTDQSE 310

Qy      265 DKIWSSYTEYVFYRE 279
      |||:||||| ||
Db      311 DKIWTSYTEYVFCRE 325
  
```

RESULT 7

AAE28628

ID AAE28628 standard; Protein; 103 AA.

XX

AC AAE28628;

XX

DT 27-DEC-2002 (first entry)

XX

DE Human K+betaM2 protein fragment.

XX

KW Human; potassium channel beta-subunit; K+betaM2 protein; neural disorder;
 KW reproductive disorder; metabolic disorder; premature puberty; nephritis;
 KW endocrine disorder; memory disorder; neuroendocrine condition; asthma;
 KW spermatogenesis; renal disease; learning deficiency; Alzheimer's disease;
 KW neurodegenerative disease; proliferative disorder; autoimmune disease;
 KW carcinoid tumour; blood coagulation disease; blood platelet disease;
 KW rheumatoid arthritis; allergy; hyperproliferative disease; gene therapy;
 KW graft-versus-host disease; organ rejection; antisterility; thrombolytic;
 KW antiinflammatory; neuroprotective; anti-Parkinsonian; immunosuppressive;
 KW nephrotropic; cytostatic; nootropic; hypotensive; vulnerary.

XX

OS Homo sapiens.

XX

PN WO200266601-A2.

XX

PD 29-AUG-2002.

XX

PF 24-JAN-2002; 2002WO-US02332.

XX
 PR 24-JAN-2001; 2001US-263872P.
 PR 14-FEB-2001; 2001US-269794P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Feder J, Lee L, Chen J, Jackson D, Ramanathan C, Siemers N;
 PI Chang H, Carroll P;
 XX
 DR WPI; 2002-691617/74.
 XX
 PT New potassium channel beta-subunit, K+betaM2, proteins and nucleic
 PT acids, useful for diagnosing, treating and/or preventing e.g.
 PT reproductive, neural, metabolic, endocrine, memory, neurodegenerative
 PT disorders or diseases -
 XX
 PS Disclosure; Page 356; 366pp; English.
 XX
 CC The present invention relates to human potassium channel beta-subunit
 CC (K+betaM2) proteins and polynucleotides encoding such proteins. The
 CC K+betaM2 sequences are useful for diagnosing, treating and/or preventing
 CC reproductive disorders, neural disorders, disorders related to aberrant
 CC potassium regulation or hyper potassium channel activity, metabolic
 CC disorders (e.g. premature puberty), endocrine disorders (e.g. aberrant
 CC growth hormone synthesis and/or secretion), memory disorder, disorders
 CC of the testis (e.g. spermatogenesis), neuroendocrine condition related
 CC to aberrant thyroid hormone release, renal disease or disorders (e.g.
 CC nephritis), disorders related to aberrant higher brain function (e.g.
 CC learning deficiencies), neurodegenerative diseases (e.g. Alzheimer's
 CC disease), proliferative disorders (e.g. carcinoid tumour) and disorders
 CC involving excessive smooth muscle tone or excitability (e.g. asthma).
 CC They may be used to modulate haemostatic or thrombolytic activity, to
 CC treat or prevent blood coagulation diseases or disorders, blood platelet
 CC diseases, wounds, autoimmune diseases, disorders or conditions (e.g.
 CC rheumatoid arthritis), allergic reactions (e.g. asthma), organ rejection
 CC or graft-versus-host disease, and hyperproliferative diseases. K+betaM2
 CC sequences are also used in gene therapy. The present sequence is human
 CC K+betaM2 protein fragment.
 XX
 SQ Sequence 103 AA;

 Query Match 23.7%; Score 541; DB 23; Length 103;
 Best Local Similarity 100.0%; Pred. No. 3.7e-46;
 Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 25 EVVELNVGGQVYFTRHSTLISIPHSLLWKMFS PKRDTANDLAKDSKGRFFIDRDGFLFRY 84
 Db 1 EVVELNVGGQVYFTRHSTLISIPHSLLWKMFS PKRDTANDLAKDSKGRFFIDRDGFLFRY 60

 Qy 85 ILDYLRDRQVVLDPDHFPEKGRLKREAEYFQLPDLVKLLTPDEI 127
 Db 61 ILDYLRDRQVVLDPDHFPEKGRLKREAEYFQLPDLVKLLTPDEI 103

 RESULT 8
 ABB60184
 ID ABB60184 standard; Protein; 228 AA.

XX
 AC ABB60184;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 7344.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI; 2001-656860/75.
 DR N-PSDB; ABL04287.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 PS Disclosure; SEQ ID NO 7344; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 228 AA;

Query Match 23.6%; Score 538.5; DB 22; Length 228;
 Best Local Similarity 44.3%; Pred. No. 2.2e-45;
 Matches 116; Conservative 44; Mismatches 61; Indels 41; Gaps 7;

Qy 24 PEVVELNVGGQVYFTRHSTLISIPHSLLWKMFS PKRDTANDLAKDSKGRFFIDRDGFLFR 83
 ||::||| | | :||: :|| ::| ||: |||||::|:|||| ||
 Db 2 PEIIELNVGGVSYTTTLATLLQDKSTLLAELFGGRDS---LAKDSKGRYFLDRDGVFLFR 58
 Qy 84 YILDYLRDRQVVLDPDHFPEKGRLLKREA EYQLPDLVKLLTPDEIKQSPDEFCHSDFEDAS 143

[illegible]

RESULT 9

ABJ10887

ID ABJ10887 standard; Protein; 228 AA.

XX

AC ABJ10887;

XX

DT 05-DEC-2002 (first entry)

XX

DE K+beta M6 related protein SEQ ID No 3.

XX

KW Cytostatic; cardiant; neuroprotective; immunomodulator; antimigraine;
KW sedative; gynaecological;; potassium channel beta subunit; K+betaM6;
KW gastrointestinal; reproductive; neural; sleep; low DNA repair capacity;
KW hyperpotassium channel activity; cardiovascular; melatonin synthesis;
KW mammary cancer tumourigenesis; pineal gland associated disorder;
KW pulmonary disorder; immune disorder; NF-kB activity; migraine headache;
KW low free-radical buffering capacity; delayed sleep phase syndrome;
KW circadian cycle; melatonin secretion; cancer.

XX

OS *Drosophila melanogaster*.

XX

PN WO200270727-A2.

XX

PD 12-SEP-2002.

XX

PF 21-FEB-2002; 2002WO-US05674.

XX

PR 21-FEB-2001; 2001US-270132P.

PR 27-MAR-2001; 2001US-278953P.

XX

PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX

PI Feder J, Lee L, Chen J, Jackson DG, Ramanathan C, Siemers N;
PI Chang H;

XX

DR WPI; 2002-713455/77.

XX

PT New polynucleotide encoding human potassium channel beta subunit
PT polypeptide, useful for diagnosing, preventing, treating or
PT ameliorating e.g. cancer -

XX

PS Disclosure; Fig 2; 332pp; English.

XX

CC The invention relates to an isolated polynucleotide encoding a potassium
CC channel beta subunit (K+betaM6) polypeptide or its variants. The human
CC potassium beta subunit polynucleotide or polypeptide is useful for
CC diagnosing, preventing, treating or ameliorating a pathological condition
CC such as gastrointestinal, reproductive, neural, sleep, cardiovascular or
CC pulmonary disorders, a disorder related to hyperpotassium channel
CC activity, an immune disorder related to aberrant NF-kB activity, pineal
CC gland associated disorders, migraine headaches, disorders associated with
CC aberrant melatonin synthesis and/or release or with low DNA repair
CC capacities or low free-radical buffering capacity, delayed sleep phase
CC syndrome, aberrations in circadian cycle, mammary cancer tumourigenesis,
CC age related disorders associated with decreased melatonin secretion, or
CC cancer. This sequence represents a potassium channel beta subunit
CC (K+betaM6) related protein of the invention.

XX

SQ Sequence 228 AA;

Query Match 23.6%; Score 538.5; DB 23; Length 228;
Best Local Similarity 44.3%; Pred. No. 2.2e-45;
Matches 116; Conservative 44; Mismatches 61; Indels 41; Gaps 7;

Qy 24 PEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPPKRDANDLAKDSKGRFFIDRDGFLFR 83
| | : | | | | | | | : | | : | | : | | : | | | | | : | : | | | |
Db 2 PEIIEELNVGGVSYTTTLATLLQDKSTLLAELFGEGRDS---LAKDSKGRYFLDRDGVLF 58

Qy 84 YILDYLRDRQVVLDPHFPEKGRLEKREAEYFQLPDLVKLLTPDEIKQSPDEFCHSDFEDAS 143
| | | : | | | : : | | : | | : | | | | | : | | : : : : :
Db 59 YILDFLRDKALHLPEGFRERQRLLEAEHFKLTAMLECI R SER----- 101

Qy 144 QGSDTRICPPSSLLPADRKWGFITVGYRGSCITLGREGQADAKFRRVPRILVCGRISLAKE 203
| | | | | | | | | | | | : | | | | | | : | | | | | : | | | | : |
Db 102 ---DAR--PP-----GCITIGYRGSFQFGKDGLADVKFRKLSRILVCGRVAQCRE 146

Qy 204 VFGETLNE SRDPDR-APERYTSR FYLKFKHLERAFDMLSECGFHMV-ACNSSVTASFINQ 261
| | | : | | | | | | | : | | | | | : | : | | | | : | | | |
Db 147 VFGDTLNE SRDPDHGGTD RYTSRFFLKH CYIEQAFDNLHDHGYRMAGSCGSGTAGSAAEP 206

Qy 262 Y----TDDKIWSSYTEYVFYRE 279
| : : | : | | : | | | :
Db 207 KPGVDTEENRWNHYNEFVFIRD 228

RESULT 10

ABJ10893

ID ABJ10893 standard; Protein; 101 AA.

XX

AC ABJ10893;

XX

DT 05-DEC-2002 (first entry)

XX

DE K+beta M6 related protein SEQ ID No 13.

XX

KW Cytostatic; cardiant; neuroprotective; immunomodulator; antimigraine;
KW sedative; gynaecological;; potassium channel beta subunit; K+betaM6;
KW gastrointestinal; reproductive; neural; sleep; low DNA repair capacity;

KW hyperpotassium channel activity; cardiovascular; melatonin synthesis;
 KW mammary cancer tumourigenesis; pineal gland associated disorder;
 KW pulmonary disorder; immune disorder; NF-kB activity; migraine headache;
 KW low free-radical buffering capacity; delayed sleep phase syndrome;
 KW circadian cycle; melatonin secretion; cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200270727-A2.
 XX
 PD 12-SEP-2002.
 XX
 PF 21-FEB-2002; 2002WO-US05674.
 XX
 PR 21-FEB-2001; 2001US-270132P.
 PR 27-MAR-2001; 2001US-278953P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Feder J, Lee L, Chen J, Jackson DG, Ramanathan C, Siemers N;
 PI Chang H;
 XX
 DR WPI; 2002-713455/77.
 XX
 PT New polynucleotide encoding human potassium channel beta subunit
 PT polypeptide, useful for diagnosing, preventing, treating or
 PT ameliorating e.g. cancer -
 XX
 PS Disclosure; Fig 1; 332pp; English.
 XX
 CC The invention relates to an isolated polynucleotide encoding a potassium
 CC channel beta subunit (K+betaM6) polypeptide or its variants. The human
 CC potassium beta subunit polynucleotide or polypeptide is useful for
 CC diagnosing, preventing, treating or ameliorating a pathological condition
 CC such as gastrointestinal, reproductive, neural, sleep, cardiovascular or
 CC pulmonary disorders, a disorder related to hyperpotassium channel
 CC activity, an immune disorder related to aberrant NF-kB activity, pineal
 CC gland associated disorders, migraine headaches, disorders associated with
 CC aberrant melatonin synthesis and/or release or with low DNA repair
 CC capacities or low free-radical buffering capacity, delayed sleep phase
 CC syndrome, aberrations in circadian cycle, mammary cancer tumourigenesis,
 CC age related disorders associated with decreased melatonin secretion, or
 CC cancer. This sequence represents a potassium channel beta subunit
 CC (K+betaM6) related protein of the invention.
 XX
 SQ Sequence 101 AA;

Query Match 16.1%; Score 367; DB 23; Length 101;
 Best Local Similarity 68.4%; Pred. No. 1.1e-28;
 Matches 67; Conservative 19; Mismatches 10; Indels 2; Gaps 1;

Qy 25 EVVELNVGGQVYFTRHSTLISIPHSLLWKMFS PKRDTANDLAKDSKGRFFIDRDGFLFRY 84
 ::||||||| || |:::| |||:|: :: :||:|||||:|||||||
 Db 1 DIVELNVGGQVYVTRRCTVVSVPDSLWWMFTQQQ--PQELARDSKGRFFLDRDGFLFRY 58
 Qy 85 ILDYLRDRQVVLDPDHFPEKGRLKREAEYFQLPDLVKLL 122
 ||||| |:|:|:|: |:|:|:|:|:|:|:|

RESULT 11

AAM25877

ID AAM25877 standard; Protein; 272 AA.

XX

AC AAM25877;

XX

DT 16-OCT-2001 (first entry)

XX

DE Human protein sequence SEQ ID NO:1392.

XX

KW Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
KW antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
KW antibacterial; endocrine; cardiant; central nervous system; virucide;
KW anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
KW antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema;
KW dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
KW genetic disease; haematopoietic disorder; platelet disorder; asthma;
KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
KW allergic rhinitis; diabetes; multiple sclerosis; depression;
KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
KW neurological disorder.

XX

OS Homo sapiens.

XX

PN WO200153455-A2.

XX

PD 26-JUL-2001.

XX

PF 22-DEC-2000; 2000WO-US35017.

XX

PR 23-DEC-1999; 99US-0471275.

PR 21-JAN-2000; 2000US-0488725.

PR 25-APR-2000; 2000US-0552317.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Tang YT, Liu C, Drmanac RT;

XX

DR WPI; 2001-457603/49.

DR N-PSDB; AAH99818.

XX

PT Isolated human polynucleotides encoding polypeptides, useful for the
PT treatment and diagnosis of e.g. cancer, ulcers and HIV infection -

XX

PS Claim 20; Page 285; 1217pp; English.

XX

CC AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
CC AAM25963. The proteins can have activities based on the tissues and
CC cells they are expressed in, such as: antiinflammatory; antirheumatic;
CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;

CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;
 CC cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary;
 CC antiulcer; osteopathic; dermatological; antiallergic; antiasthmatic;
 CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
 CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides
 CC encoding them can be used in gene therapy, antisense therapy and vaccine
 CC production, The proteins and polynucleotides are useful for screening for
 CC agonists or antagonists of a protein and for the treatment and diagnosis
 CC of disorders associated with the activity of a protein e.g. inflammation,
 CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
 CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
 CC infections, autoimmunity, genetic diseases, haematopoietic disorders,
 CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
 CC osteoporosis, severe combined immunodeficiency, eczema, allergic
 CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
 CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
 CC neurological disorders.
 XX
 SQ Sequence 272 AA;

Query Match 10.2%; Score 232; DB 22; Length 272;
 Best Local Similarity 42.6%; Pred. No. 1.9e-14;
 Matches 52; Conservative 23; Mismatches 39; Indels 8; Gaps 2;

QY 12 PREQGSAPVNSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSKRDNTANDLAKDSKG 71
 | | | : : : ||||| : | | : | | | | : | | | | : || : |
 Db 17 PATQSPAM----SDPITLVNKGKLYTTSLATLTSFPDSMLGAMFSGKMPT----KRDSQG 68
 QY 72 RFFIDRDGFLFRYILDYLRDRQVLPDHFPEKGRLEAEYFQLPDLVKLLTPDEIKQSP 131
 ||||| : ||||| : || : || : | | | | : ||| : : | : | : | : |
 Db 69 NCFIDRDGKVFRIYILNFLRTSHLDLPEDFQEMGLLRREADFYQVQPLIEALQEKEVELSK 128
 QY 132 DE 133
 |
 Db 129 AE 130

RESULT 12

ABP69573

ID ABP69573 standard; Protein; 290 AA.

XX

AC ABP69573;

XX

DT 20-JAN-2003 (first entry)

XX

DE Human polypeptide SEQ ID NO 1620.

XX

KW Human; genome mapping; gene therapy; food supplement; virus; fungus;

KW cell-proliferative disorder; neurodegenerative disease; bacterial;

KW Parkinson's disease; Alzheimer's disease; autoimmune disease;

KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;

KW arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;

KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;

KW haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;

KW antiarthritic.

XX

OS Homo sapiens.

XX
 PN WO200270539-A2.
 XX
 PD 12-SEP-2002.
 XX
 PF 05-MAR-2002; 2002WO-US05095.
 XX
 PR 05-MAR-2001; 2001US-0799451.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
 PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
 PI Wehrman T, Wang J, Wang D, Drmanac RT;
 XX
 DR WPI; 2002-759812/82..
 DR N-PSDB; ABZ11790.
 XX
 PT New polynucleotides comprising sequences assembled from expressed
 PT sequence tags (ESTs), useful for treating cell-proliferative,
 PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or
 PT platelet or coagulation disorders -
 XX
 PS Claim 9; SEQ ID NO 1620; 1012pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated polynucleotide (I) comprising a
 CC nucleotide sequence selected from any of 948 sequences
 CC (ABZ11119-ABZ12066) or their mature protein coding portion, active domain
 CC coding protein or complementary sequences. The polynucleotides are useful
 CC for identifying expressed genes or for physical mapping of human genome.
 CC The encoded polypeptides (ABP68902-ABP69849) are useful as molecular
 CC weight markers, as a food supplement, for generating antibodies, in
 CC medical imaging, screening and diagnostic assays and for treating
 CC cell-proliferative disorders (cancer), neurodegenerative diseases
 CC (Parkinson's or Alzheimer's disease), autoimmune diseases (multiple
 CC sclerosis, diabetes, lupus) genetic disorders, myeloid or lymphoid
 CC disorders, platelet or coagulation disorders, wound, burns, incision,
 CC ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal,
 CC parasitic), arthritis, etc.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 290 AA;

Query Match 10.1%; Score 231; DB 23; Length 290;
 Best Local Similarity 45.8%; Pred. No. 2.7e-14;
 Matches 49; Conservative 21; Mismatches 33; Indels 4; Gaps 1;

Qy 27 VELNVGGQVYFTRHSTLISIPHSLWKMFSKPRDTANDLAKDSKGRFFIDRDGFLFRYIL 86
 : ||||:| | :|| | | |:| ||| | | :||:| ||||| :|||
 Db 5 ITLNVGGKLYTTSLATLTSFPDMLGAMFSGKMPT----KRDSQGNCFIDRDGKVFYIL 60
 Qy 87 DYLRDRQVVLDPDHFPEKGRLEAEYFQLPDLVKLLTPDEIKQSPDE 133
 :||| :||: | | | |:||:|:| :||: | | :||: | |
 Db 61 NFLRTSHLDLPEDFQEMGLLRREADFYQVQPLIEALQEKEVELSKAE 107

RESULT 13

AAE10329

ID AAE10329 standard; Protein; 339 AA.

XX

AC AAE10329;

XX

DT 10-DEC-2001 (first entry)

XX

DE Human transporter and ion channel-6 (TRICH-6) protein.

XX

KW Human; transporter and ion channel; TRICH-6; therapy; akinesia; cardiant;
 KW neurological disorder; immune disorder; allergy; nootropic; dementia;
 KW AIDS; Acquired Immune Deficiency Syndrome; amyotrophic lateral sclerosis;
 KW cystic fibrosis; Alzheimer's disease; depression; epilepsy; scleroderma;
 KW cardiomyopathy; muscular dystrophy; Crohn's disease; multiple sclerosis;
 KW rheumatoid arthritis; cancer; anaemia; asthma; trauma; haemodialysis;
 KW gastritis; inflammation; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1..32

FT /label= Signal_peptide

FT Protein 33..339

FT /label= Mature_TRICH_6_protein

XX

PN WO200162923-A2.

XX

PD 30-AUG-2001.

XX

PF 23-FEB-2001; 2001WO-US05942.

XX

PR 25-FEB-2000; 2000US-0184866.

PR 02-MAR-2000; 2000US-0187947.

PR 09-MAR-2000; 2000US-0188333.

PR 17-MAR-2000; 2000US-0190230.

PR 24-MAR-2000; 2000US-0192077.

PR 30-MAR-2000; 2000US-0193500.

XX

PA (INCY-) INCYTE GENOMICS INC.

XX

PI Yue H, Tang YT, Lal P, Policky JL, Nguyen DB, Au-Young J, Yao MG;
 PI Khan FA, Walia NK, Gandhi AR, Tribouley CM, Patterson C;
 PI Thornton M, Greene BD, Hernandez R, Borowsky ML, Sanjanwala MS;

XX

DR WPI; 2001-582050/65.

DR N-PSDB; AAD17473.

XX

PT Thirteen human transporters and ion channels (referred to as TRICH-1 to
 PT TRICH-13), useful in the diagnosis, treatment and prevention of
 PT transport (e.g. akinesia), neurological, muscle or immunological
 PT disorders (e.g. allergies) -

XX

PS Claim 1; Page 111; 131pp; English.

XX

CC The present sequence is human transporters and ion channels

CC (TRICH-6) protein. The TRICH DNA, protein and their agonist and
CC antagonists are useful in the diagnosis, treatment and prevention of
CC transport disorders (akinesia, amyotrophic lateral sclerosis, cystic
CC fibrosis), neurological (Alzheimer's disease, dementia, depression,
CC epilepsy), muscle (e.g. cardiomyopathy, Becker's muscular dystrophy) or
CC immunological disorders (e.g. allergies, acquired immunodeficiency
CC syndrome (AIDS), Crohn's disease, rheumatoid arthritis, scleroderma,
CC multiple sclerosis), viral, bacterial, parasitic, protozoal and
CC helminthic disorders, cancer, anaemia, asthma, trauma, haemodialysis,
CC gastritis and inflammation.

XX

SQ Sequence 339 AA;

Query Match 10.1%; Score 231; DB 22; Length 339;

Best Local Similarity 45.8%; Pred. No. 3.4e-14;

Matches 49; Conservative 21; Mismatches 33; Indels 4; Gaps 1;

Qy 27 VELNVGGQVYFTRHSTLISIPHSLLWKMFSFKRDTANDLAKDSKGRFFIDRDGFLFRYIL 86
: |||||::| | :|| | | |:| ||| | | :||:| ||||| :|||

Db 5 ITLNVGGKLYTTSLATLTSFPDSMLGAMFSGKMPT----KRDSQGNCFIDRDGKVFYRIL 60

Qy 87 DYLRDRQVVLDPDHFPEKGRLLKREAEYFQLPDLVKLLTPDEIKQSPDE 133
::|| : ||: | | | |:|||::|: |:: | |:: | |

Db 61 NFLRTSHLDLPEDFQEMGLLRREADFYQVQPLIEALQEKEVELSKAE 107

RESULT 14

AAB41802

ID AAB41802 standard; Protein; 283 AA.

XX

AC AAB41802;

XX

DT 08-FEB-2001 (first entry)

XX

DE Human ORFX ORF1566 polypeptide sequence SEQ ID NO:3132.

XX

KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KW vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW cholesterol ester storage; systemic lupus erythematosus; infection;
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW thrombosis; contraceptive.

XX

OS Homo sapiens.

XX

PN WO200058473-A2.

XX

PD 05-OCT-2000.

XX

PF 31-MAR-2000; 2000WO-US08621.
XX
PR 31-MAR-1999; 99US-0127607.
PR 02-APR-1999; 99US-0127636.
PR 05-APR-1999; 99US-0127728.
PR 30-MAR-2000; 2000US-0540763.

XX
PA (CURA-) CURAGEN CORP.

XX
PI Shimkets RA, Leach M;

XX
DR WPI; 2000-602362/57.
DR N-PSDB; AAC76011.

XX
PT Novel nucleic acids and peptides derived from open reading frame X,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease -

XX
PS Claim 11; Page 2349-2350; 5507pp; English.

XX
CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC which represent the human OREFX open reading frames 1 to 3161. The OREFX
CC sequences have activities such as: cytostatic; hepatotropic; vulnerary;
CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
CC antidiabetic; hypotensive; dermatological; immunosuppressive;
CC antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
CC antithyroid; and antianaemic. The sequences can be used for determining
CC the presence of or predisposition to, or preventing or treating
CC pathological conditions associated with an OREFX-associated disorder. The
CC nucleic acids can be used to express OREFX proteins in gene therapy
CC vectors. The proteins and nucleic acids may be used to treat cancers,
CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
CC graft vs host disease, cardiovascular disease, diabetes mellitus,
CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
CC coagulation; to inhibit thrombosis; and as a contraceptive.

XX
SQ Sequence 283 AA;

Query Match 9.2%; Score 210.5; DB 21; Length 283;
Best Local Similarity 28.3%; Pred. No. 2.9e-12;
Matches 80; Conservative 41; Mismatches 89; Indels 73; Gaps 13;

Qy 15 QGSAVPNSFPE---VVELNVGGQVYFTRHSTLISIPHSLLWKMFSKRDANDLAKDS-K 70
|| :| : |::|| :| : :|| | | : :| | : || |
Db 43 QGIPLPAQLTKSNAPVHIDVGGHMYTSSLATLTKYPESRIGRLF----DGTEPIVLDSLK 98

Qy 71 GRFFIDRDGFLFRYILDYLRDRQVVLDPHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQS 130
:||||| :|||||::|| :::|| | : | ||:|||| : || : ||
Db 99 QHYFIDRDGQMFYILNFLRTSKLLIPDDFKDYTLLEYEAKYFQLQPM--LLEMERWKQ- 155

Qy 131 PDEFCHSDFEDASQGS DTRICPPSSLLPADRKWGFITVGYRG SCTLGREGQADAKFRRVP 190

```

      |   |   :| |   : | : ||
Db      156 -----DRETGRFSRPCE-----CLVVRVAPDLGE----- 179
Qy      191 RILVCGRISLAKEVFGE-----TLNESRDPDRAPERYTSRFYLK-FKHLE--RAFDML 240
      || : | || :||| |   :| : |   : || | : || : : |
Db      180 RITLSGDKSLIEEVFPEIGDVMCNSVNAGWNHD---STHVIRFPLNGYCHLNSVQVLERL 236
Qy      241 SECGFHMV-ACNSSVTASFINQYTDDKIWSSYTEYVFYREPSR 282
      : || :| :| | :   | :||| || |
Db      237 QQRGFEIVGSCGGGVDS-----SQFSEYVLRRELRR 267

```

RESULT 15

AAAY34125

ID AAY34125 standard; Protein; 256 AA.

XX

AC AAY34125;

XX

DT 30-NOV-1999 (first entry)

XX

DE Human potassium channel K+Hnov27.

XX

KW Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;
 KW cardiovascular disorder; CNS disorder; renal disorder.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 15

FT /label= Ile, Asn

FT /note= "Encoded by AWC"

XX

PN WO9943696-A1.

XX

PD 02-SEP-1999.

XX

PF 22-FEB-1999; 99WO-US03826.

XX

PR 19-JAN-1999; 99US-0116448.

PR 25-FEB-1998; 98US-0076687.

PR 07-AUG-1998; 98US-0095836.

XX

PA (AXYS-) AXYS PHARM INC.

XX

PI Curran ME, Hu P, Miller AP, Rutter M, Wang J;

XX

DR WPI; 1999-527591/44.

DR N-PSDB; AAZ11903.

XX

PT New nucleic acids encoding mammalian K+Hnov potassium channel
 PT proteins, useful for the diagnosis and treatment of episodic ataxia
 PT with myokymia, cardiac arrhythmia, epilepsy and Bartter's syndrome

XX

PS Claim 3; Page 66; 112pp; English.

XX

CC This sequence represents the human K+Hnov27 potassium channel.

CC K+Hnov proteins have a high degree of homology to known potassium

CC channels and may be alpha subunits, which form the functional channel,
 CC or accessory subunits that act to modulate the channel activity.
 CC K+Hnov27 is a potassium channel modulatory subunit. The gene's
 CC chromosomal location is 18q12, determined via PCR
 CC chromosomal localisation. K+Hnov cDNAs were isolated
 CC by extension of expressed sequence tags (ESTs) which were
 CC related but not identical to known human potassium channels. Potential
 CC polymorphisms detected as sequence variants between multiple
 CC independent clones. Potassium channels have critical roles in various
 CC cell types and biochemical pathways. Defective potassium channels are
 CC known to cause four human diseases: episodic ataxia with myokymia;
 CC cardiac arrhythmia (long QT syndrome); epilepsy; and Bartter's syndrome.
 CC As potassium channels are critical components of virtually all cells,
 CC it is likely that abnormal potassium channels are also implicated in
 CC certain renal, cardiovascular and central nervous system (CNS) disorders.
 CC Nucleotides encoding K+Hnov proteins may be used for identifying
 CC homologous or related proteins and the DNA sequences encoding them. They
 CC may be used to produce compositions that modulate the expression and
 CC function of the K+Hnov protein and in studying the biochemical pathways
 CC associated with it. They may also be used for the recombinant production
 CC of K+Hnov protein in fermentation cultures. Additionally, such
 CC nucleotides may be used in gene therapy protocols for the treatment
 CC of diseases associated with abnormal potassium channels.

XX

SQ Sequence 256 AA;

Query Match 9.2%; Score 210; DB 20; Length 256;

Best Local Similarity 28.7%; Pred. No. 2.8e-12;

Matches 77; Conservative 39; Mismatches 82; Indels 70; Gaps 12;

```

Qy      27 VELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDS-KGRFFIDRDGFLFRYI 85
      |::|||:|:|:| | | :::| | : || | :||| | :|||
Db      32 VHIDVGGHMYTSSLATLTYPESRIGRLF----DGTEPIVLDSLKQHYFIDRDGQMFRYI 87

Qy      86 LDYLRDRQVVLDPDHFPEKGRLKREAEIFQLPDLVKLLTPDEIKQSPDEFCHSDFEDASQG 145
      |::|| ::::| | : | ||:| | | : || : || | |
Db      88 LNFLRTSKLLIPDDFKDYTLTYEEAKYFQLQPM--LLEMERWKQ-----DRETG 134

Qy     146 SDTRICPPSSLLPADRKWGFITVGYRGSCITLGREGQADAKFRRVPRILVCGRISLAKEVF 205
      :| | : | : || | | : | ||:| |
Db     135 RFSRPCE-----CLVVRVAPDLGE-----RITLSGDKSLIEEVF 168

Qy     206 GE-----TLNESRDPDRAPERYTSRFYLYK-FKHLE--RAFDMLSECGFHMV-ACNSSV 254
      | :| :| : | || | : || : | : || :| :|
Db     169 PEIGDVMCNSVNAGWNHD---STHVIRFPLNGYCHLNSVQVLERLQQRGFVIGSCGGGV 225

Qy     255 TASFINQYTDCKIWSSYTEYVFYREPSR 282
      : | :||| || |
Db     226 DS-----SQFSEYVLRRELRR 241

```

Search completed: January 29, 2004, 02:52:25

Job time : 57 secs

OM protein - protein search, using sw model

Run on: January 29, 2004, 02:51:31 ; Search time 23 Seconds
(without alignments)
787.350 Million cell updates/sec

Title: US-10-056-884A-2
Perfect score: 2284
Sequence: 1 MALSGNCSRYYPREQSAVP.....DRFPERKHPWQSELLRKYHL 428

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	210	9.2	256	4	US-09-336-643A-14	Sequence 14, Appl
2	202.5	8.9	237	4	US-09-336-643A-25	Sequence 25, Appl
3	189	8.3	258	4	US-09-336-643A-12	Sequence 12, Appl
4	146.5	6.4	812	4	US-09-166-350-12	Sequence 12, Appl
5	133.5	5.8	389	4	US-09-336-643A-27	Sequence 27, Appl
6	106	4.6	646	4	US-09-336-643A-10	Sequence 10, Appl
7	100.5	4.4	162	2	US-08-606-143-44	Sequence 44, Appl
8	100	4.4	490	4	US-09-336-643A-6	Sequence 6, Appli
9	95.5	4.2	499	4	US-09-336-643A-8	Sequence 8, Appli
10	95	4.2	1384	3	US-08-976-255-11	Sequence 11, Appl
11	94.5	4.1	3287	2	US-08-477-451-7	Sequence 7, Appli

12	92.5	4.0	848	3	US-08-976-255-10	Sequence 10, Appl
13	92	4.0	393	4	US-09-252-991A-25633	Sequence 25633, A
14	92	4.0	636	4	US-09-142-791A-2	Sequence 2, Appli
15	92	4.0	636	4	US-09-178-109-4	Sequence 4, Appli
16	92	4.0	655	4	US-09-142-791A-4	Sequence 4, Appli
17	92	4.0	655	4	US-09-178-109-2	Sequence 2, Appli
18	92	4.0	768	2	US-08-408-519-2	Sequence 2, Appli
19	92	4.0	768	5	PCT-US95-03552-2	Sequence 2, Appli
20	91.5	4.0	664	3	US-09-295-186-17	Sequence 17, Appl
21	91	4.0	580	3	US-08-482-677-10	Sequence 10, Appl
22	90.5	4.0	352	4	US-09-328-352-8196	Sequence 8196, Ap
23	89.5	3.9	2289	3	US-09-051-019-2	Sequence 2, Appli
24	87.5	3.8	1065	4	US-09-221-013A-10	Sequence 10, Appl
25	86.5	3.8	601	4	US-09-336-643A-4	Sequence 4, Appli
26	86.5	3.8	685	3	US-08-960-048-7	Sequence 7, Appli
27	86.5	3.8	685	4	US-09-838-586-7	Sequence 7, Appli
28	86.5	3.8	1317	3	US-09-083-521-7	Sequence 7, Appli
29	86	3.8	296	4	US-07-757-022B-70	Sequence 70, Appl
30	86	3.8	528	2	US-08-527-152-2	Sequence 2, Appli
31	86	3.8	875	4	US-09-328-352-4884	Sequence 4884, Ap
32	84.5	3.7	1471	3	US-08-755-587-188	Sequence 188, App
33	84	3.7	190	2	US-08-606-143-37	Sequence 37, Appl
34	84	3.7	208	2	US-08-606-143-40	Sequence 40, Appl
35	84	3.7	448	1	US-08-295-411-3	Sequence 3, Appli
36	84	3.7	448	2	US-08-955-471-3	Sequence 3, Appli
37	84	3.7	448	5	PCT-US92-10242-3	Sequence 3, Appli
38	84	3.7	636	4	US-09-142-791A-6	Sequence 6, Appli
39	84	3.7	881	3	US-08-960-048-8	Sequence 8, Appli
40	84	3.7	881	4	US-09-838-586-8	Sequence 8, Appli
41	83.5	3.7	159	2	US-08-606-143-45	Sequence 45, Appl
42	83.5	3.7	339	1	US-08-248-629A-5	Sequence 5, Appli
43	83.5	3.7	339	1	US-08-451-932-5	Sequence 5, Appli
44	83.5	3.7	339	1	US-08-452-260-5	Sequence 5, Appli
45	83.5	3.7	339	1	US-08-326-785-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1

US-09-336-643A-14

; Sequence 14, Application US/09336643A

; Patent No. 6399761

; GENERAL INFORMATION:

; APPLICANT: Miller, Andrew P.

; APPLICANT: Curran, Mark Edward

; APPLICANT: Hu, Ping

; APPLICANT: Rutter, Marc

; APPLICANT: Wang, Jian-Wang

; TITLE OF INVENTION: No. 6399761el Human Potassium Channels

; FILE REFERENCE: SEQ-15P

; CURRENT APPLICATION NUMBER: US/09/336,643A

; CURRENT FILING DATE: 1999-06-18

; PRIOR APPLICATION NUMBER: 60/076,687

; PRIOR FILING DATE: 1998-08-07

; PRIOR APPLICATION NUMBER: 60/116,448

; PRIOR FILING DATE: 1999-01-19


```
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 256
;   TYPE: PRT
;   ORGANISM: H. sapiens
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)...(256)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-09-336-643A-14
```

RESULT 2

; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 237
; TYPE: PRT
; ORGANISM: H. sapiens
US-09-336-643A-25

Query Match 8.9%; Score 202.5; DB 4; Length 237;
Best Local Similarity 39.0%; Pred. No. 1.2e-12;
Matches 48; Conservative 22; Mismatches 44; Indels 9; Gaps 2;

Qy 27 VELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDANDLAKDSKGRFFIDRDGFLFRYIL 86
| | | | | : | | : | | | | : | | | | | | | | : |
Db 14 VTLNVGGHLYTTSLTTLTRYPDMSLGAMFGGDFPT----ARDPQGNFYIDRDGPLFRYVL 69

Qy 87 DYLRDRQVVLDPDHFPEKGRLLKREAIFYQLPDLVKLLTPDEIKQSPDEFCHSDFEDASQGS 146
: : | | : : | | | | | : : | | : : | | : : |
Db 70 NFLRTSELTLPLDFKEFDLLRKEADFYQIEPLIQCLNDPKPLYPMD-----TFEEVVVELS 124

Qy 147 DTR 149
| |
Db 125 STR 127

RESULT 3

US-09-336-643A-12

; Sequence 12, Application US/09336643A
; Patent No. 6399761
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. 6399761el Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643A
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 258
; TYPE: PRT
; ORGANISM: H. sapiens
US-09-336-643A-12

Query Match 8.3%; Score 189; DB 4; Length 258;
Best Local Similarity 34.7%; Pred. No. 3.2e-11;

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Matches    51;  Conservative    24;  Mismatches    40;  Indels    32;  Gaps    6;

Qy          14  EQGSVPNSFPEVVVELNVGGQVYFTRHSTLISIPHSLL-----WKMFS PKRDTANDLAKD  68
              :||      |      :: ||||| :| |: ||      | : |      | : |      |
Db          25  DQGK---NCKSTLMTLNVGGYLYITQKQTLTKYPDTFLEGIVNGKILCP-----FD  72

Qy          69  SKGRFFIDRDGFLFRYILDYLRDRQVVLDPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIK  128
              : | :||| || ||::||:|: ::||: | |      | :||: || |      | :|:|
Db          73  ADGHYFIDRDGLLFRHVLNFLRNGELLPEGFRENQLLAQEAEFFQLKGLA-----EEVK  127

Qy          129  Q-----SPDEFCH---SDFEDASQG  145
              :| |      :| | |||
Db          128  SRWEKEQLTPRETTFLEITDNHDSRSG  154

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RESULT 4

US-09-166-350-12

; Sequence 12, Application US/09166350A

; Patent No. 6440663

; GENERAL INFORMATION:

; APPLICANT: Scanlan, Matthew

; APPLICANT: Chen, Yao

; APPLICANT: Stockert, Elisabeth

; APPLICANT: Old, Lloyd

; APPLICANT: Jager, Elke

; APPLICANT: Knuth, Alex

; TITLE OF INVENTION: Renal Cancer Associated Antigens and

; TITLE OF INVENTION: Uses Therefor

; FILE REFERENCE: L0461/7051

; CURRENT APPLICATION NUMBER: US/09/166,350A

; CURRENT FILING DATE: 1998-10-05

; EARLIER APPLICATION NUMBER: US 09/166,350

; EARLIER FILING DATE: 1998-10-05

; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 12

; LENGTH: 812

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-166-350-12

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Query Match          6.4%;  Score 146.5;  DB 4;  Length 812;
Best Local Similarity 32.8%;  Pred. No. 4.5e-06;
Matches    43;  Conservative    24;  Mismatches    43;  Indels    21;  Gaps    5;

Qy          5  GNCSRYYPREQGSVPNSFPEVVVELNVGGQVYFTRHSTLISIPHSLLWKMFS PKRDTAND  64
              |:| :      ||      |:|:||||| :| ||: || |      |:| : |
Db          4  GHCGSFPAAGSG-----EIVQLNVGGTREFSTSRQTLMWIPDSFFSSLLSGRIST---  54

Qy          65  LAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLDPDHFPEKG----RLKREAEYFQLPDLV-  119
              :| | ||||| | ||::|| ::| :|      |: |||:: : ||
Db          55  -LRDETGAIFIDRDPAAFAPILNFLRTKELDL-----RGVSINVL RHEAEFYGITPLVR  107

Qy          120  KLLTPDEIKQS  130
              :|| :|::|
Db          108  RLLCEELERS  118

```

RESULT 5

US-09-336-643A-27

```
; Sequence 27, Application US/09336643A
; Patent No. 6399761
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. 6399761el Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643A
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 389
; TYPE: PRT
; ORGANISM: H. sapiens
US-09-336-643A-27
```

```
Query Match          5.8%; Score 133.5; DB 4; Length 389;
Best Local Similarity 33.3%; Pred. No. 3.3e-05;
Matches 45; Conservative 17; Mismatches 48; Indels 25; Gaps 5;
```

```
Qy      29 LNVGGQVYFTRHSTLIS-IPHSLIWKMFSKRDRTANDLAKDSKGRFFIDRDGFLFRYILD 87
      |||||: : | |||: : | |:| || | :| :| | || | ||:
Db      93 LNVGGRYFTTTRSTLVNKEPDSMLAHMFKDKGVWGN--KQDHRGAFLIDRSPEYFEPILN 150

Qy      88 YLRDRQVVLDPDHFPEKGRCLKREAEIFQLPDLVKLLTPDEIKQSPDEFCHSDFEDASQGS 147
      ||| |::: | | |: || :| : |:: | | : |
Db     151 YLRHGQLIVNDGINLLGVLE-EARFFGIDSLIEHL-----EVAIKNSQ 192

Qy     148 TRICPPSSLLPADRK 162
      || | ||
Db     193 ----PPEDHSPISRK 203
```

RESULT 6

US-09-336-643A-10

```
; Sequence 10, Application US/09336643A
; Patent No. 6399761
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. 6399761el Human Potassium Channels
```

```
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643A
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 646
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(646)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-336-643A-10
```

```
Query Match          4.6%; Score 106; DB 4; Length 646;
Best Local Similarity 21.8%; Pred. No. 0.049;
Matches    65; Conservative    36; Mismatches    87; Indels    110; Gaps    13;
```

```
Qy      26 VVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFLFRYI 85
      |: :|| |: : | :|| | :|| | ::: | :| ||| :|::
Db      41 VLVNVSGRRFETWKNTLD RYPTLLG---SSEKEFFYDA---DSGEYFFDRDPDMFRHV 94

Qy      86 LDYLRDRQVVLDPDHFPEKGRLKRAE----YFQLPDLVKLLTPDEIKQSPDEFCH--SDF 139
      |:: | :: | | : :: | | :|:| | :| : | ::
Db      95 LNFYRTGRL----HCPRQECIQAFDEELAFYGLVPELVGDCCLEEYDRKKENAERLAED 150

Qy     140 EDASQGS DTRICPPSSLLPADRKW-----GFI-----TVG 169
      |:| | | | | | | | | | | | | | | | | | | | | |
Db     151 EEAEQAGDGPALPAGSSL-RQLRWRAFENPHTSTAALVFYYVTGFFIAVSVIANVVETIP 209

Qy     170 YRG SCTLGREGQADAKFRRVPRILVCGRISLAKEVFGETL NESRDPDRAPER YTSRFY-- 227
      ||| | | | | | | | | | | | | | | | | | | | | |
Db     210 CRGSA-----RRSSREQPCG-----ERFPQAFFCM 234

Qy     228 -----LKF--KHLERAFDMLSECGF-----H MVACNSSVTASFI 259
      | | :| | | | | | | | | | | | | | | | | | | |
Db     235 DTACVLIFTGEYLLRLFAAPSR CRFLRSVMSLIDVVAILPYYIGLLVPKNDDVSGAFV 292
```

RESULT 7

US-08-606-143-44

```
; Sequence 44, Application US/08606143
; Patent No. 5856155
; GENERAL INFORMATION:
; APPLICANT: Li, Min
; TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
; TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
; TITLE OF INVENTION: COMPOUNDS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
```

```

;   ADDRESSEE:  Leydig, Voit & Mayer, Ltd.
;   STREET:     Two Prudential Plaza, Suite 4900
;   CITY:       Chicago
;   STATE:      IL
;   COUNTRY:    USA
;   ZIP:        60601
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER:   IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE:   PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/606,143
;   FILING DATE:       23-FEB-1996
;   CLASSIFICATION:    514
;   ATTORNEY/AGENT INFORMATION:
;   NAME:             Kilyk Jr., John
;   REGISTRATION NUMBER: 30763
;   REFERENCE/DOCKET NUMBER: 71756
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:        (312) 616-5600
;   TELEFAX:          (312) 616-5700
;   TELEX:            25-3533
;   INFORMATION FOR SEQ ID NO: 44:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:          162 amino acids
;   TYPE:            amino acid
;   STRANDEDNESS:    single
;   TOPOLOGY:        linear
;   MOLECULE TYPE:    protein
US-08-606-143-44

```

```

Query Match          4.4%; Score 100.5; DB 2; Length 162;
Best Local Similarity 26.9%; Pred. No. 0.022;
Matches   39; Conservative   28; Mismatches   61; Indels   17; Gaps    6;

```

```

Qy      25 EVVELNVGGQVYFTRHSTLISIPHSLLWKMFS PKRDTANDLAKDSKGRFFIDRDGFLFRY 84
      ||: :|| |: : | :|| | :|| | :: | | :| ||| :||:
Db      2 EVLVVNVSGRRFETWKNTLDRYPDTLG---SSEKEFFYDA---ESGEYFFDRDPDMFRH 55

Qy      85 ILDYLRDRQVVLDPHFPEKGRLKREAE----YFQLPDLVKLLTPDEIKQSPDEFCH--SD 138
      :|:: | :: | | : :: | | :|:| | :| : | ::
Db      56 VLNFYRTGRL----HCPRQECIQAFDEELAFYGLVPELVGDCCLEEYDRKKEAERLAE 111

Qy      139 FEDASQGS DTRICPPSSLLPADRKW 163
      |:| | : | | | |
Db      112 DEEAEQAGEGPALPAGSSL-RQRLW 135

```

RESULT 8

US-09-336-643A-6

```

; Sequence 6, Application US/09336643A
; Patent No. 6399761
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping

```

```
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. 6399761el Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643A
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 490
; TYPE: PRT
; ORGANISM: H. sapiens
US-09-336-643A-6
```

```
Query Match          4.4%; Score 100; DB 4; Length 490;
Best Local Similarity 25.4%; Pred. No. 0.13;
Matches 35; Conservative 28; Mismatches 61; Indels 14; Gaps 5;
```

```
Qy      20 PNSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTA-----NDLAKDSKGRFF 74
      |  |:| ||||  |||: ||: | |: :  :|  |: :  |  ::
Db      10 PGQDEELVNLNVGGFKQSVQSTLLRFPHTRLGKLLTCHSEEAILLELCDDYSVADK-EYY 68

Qy      75 IDRDGFLFRYILDYLRDRQVVLDPHFPEK---GRLKREAEYFQLPDL-VKLLTPDEIKQS 130
      ||: ||||:|::  ::  | |:  :| ||: : :| :  :  ::
Db      69 FDRNPSLFRYVLNFFYTGKL----HVMEELCVFSFCQEIEYWGINELFIDSCCSNRYQER 124

Qy     131 PDEFCHSDFEDASQGSdT 148
      :|  |:: |  |
Db     125 KEENHEKDWDQKSHDVST 142
```

RESULT 9

US-09-336-643A-8

```
; Sequence 8, Application US/09336643A
; Patent No. 6399761
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. 6399761el Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643A
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
```

; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 499
; TYPE: PRT
; ORGANISM: H. sapiens
US-09-336-643A-8

Query Match 4.2%; Score 95.5; DB 4; Length 499;
Best Local Similarity 23.5%; Pred. No. 0.4;
Matches 47; Conservative 24; Mismatches 72; Indels 57; Gaps 9;

```
Qy      15 QGSAVPNSFPEVVVELNVGGQVYFTRHSTLISIPHSLLWKMF-----SPK 58
          :|  | : : :| || :  |  ||: | |:  ||
Db      29 EGEGEPLALGDCFTVNVGGSRFVLSQQALSCFPHTRLGKLAVVVASYRRPGALAAVPSPL 88

Qy      59 R--DTANDLAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLDPHFPEKGRLKR----- 108
          | || : : :| ||  ||:| | | : : : :  |:
Db      89 ELCDDANPVDNE----YFFDRSSQAFRYVLHYRTGRLVHMEQLCALSFLQEIQYWGIDE 144

Qy      109 -----EAEYFQLPDLVKLLTPDEIKQSPD-EFCHSDFEDASQGS DTRICP----- 152
          ||: :| : | | : | | :| ||  ||
Db      145 LSIDSCCRDRYFRRKELSETL--DFKKDTEDESQHESEQDFSQGP----CPTVRQKLWN 198

Qy      153 ----PSSLLPADRKWGFITV 168
          | |  | | :| |::
Db      199 ILEKPGSSTAA-RIFGVISI 217
```

RESULT 10

US-08-976-255-11

; Sequence 11, Application US/08976255
; Patent No. 6136581
; GENERAL INFORMATION:
; APPLICANT: Jono, Keith E.
; APPLICANT: Plowman, Gregory
; TITLE OF INVENTION: KINASE GENES AND USES
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,255
; FILING DATE: No. 6136581ember 21, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:


```

; APPLICATION NUMBER: 60/031,675
; FILING DATE: No. 6136581ember 22, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 229/182
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1384 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-976-255-11

```

```

Query Match          4.2%; Score 95; DB 3; Length 1384;
Best Local Similarity 30.1%; Pred. No. 2.1;
Matches 46; Conservative 20; Mismatches 55; Indels 32; Gaps 8;

```

```

Qy      288 CDCCCKNGKGDKEGESGTSCNDLSTSSCDSQSEASSPQETVICGPVTRQTNIQTLDRIK 347
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      61 CLCCKKGGIGFKEFE-----NAEGEEYVADFSEQGSPAATVQNGPDVYVLPPLTEVSLPMA 115

Qy      348 KGP---VQLIQQSEMRKSDLLRI-----LTSGSRESNMSSKKKAVKE---KLSI 391
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      116 KQPGRSVQLLKSTDVGRHS--LLYLKEIGRGWFGKVFLGEVNSGISSAQVVVKELQASASV 174

Qy      392 EEELEKCIQDFLKKKIPDRFPERKHPWQSELLR 424
          : | : : | | : | | | | | | | | | | | | | | | | | | | | | | |
Db      175 QEQM-----FLEEVQPYR--ALKH---SNLLQ 197

```

RESULT 11

US-08-477-451-7

```

; Sequence 7, Application US/08477451
; Patent No. 5928865
; GENERAL INFORMATION:
; APPLICANT: Covacci, Antonello
; TITLE OF INVENTION: Helicobacter Pylori Cagi Region
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

```

```

; APPLICATION NUMBER: US/08/477,451
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McClung, Barbara G.
; REGISTRATION NUMBER: 33,113
; REFERENCE/DOCKET NUMBER: 0335.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-601-2708
; TELEFAX: 510-655-3542
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3287 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-477-451-7

```

```

Query Match          4.1%; Score 94.5; DB 2; Length 3287;
Best Local Similarity 20.8%; Pred. No. 8.8;
Matches 93; Conservative 57; Mismatches 170; Indels 127; Gaps 19;

```

```

Qy      42 TLISIPHSLLWKMFSKP-----RDTA--NDLAK-----DSKGRFF- 74
      |||:  ||  | |:  :|  ||| |  : | |||
Db      1896 TLISLGLFLLVFRFQPETIKKYIKDPKDLQFYNDLRKKNQWDKVVYSMMSVAEQKRRFFK 1955

Qy      75 ---IDRDGFLFRYILDYLRDRQVVLDPHFPEKGRLKREAEYFQLPD-----LVKL 121
      :  :  | |  | |  | :| |:|  : :: |  ||
Db      1956 LSSACMNSIKILFFLIYSSDFQF-----ERKRMK---FFTRITDSYKKVVVTLGLVVT 2005

Qy      122 LTPDEIKQSPDEFCHSDFEDASQGS DTRICPPSSLLPADRKWGFITVGYRG SCTLGREGQ 181
      |  || |  |::|  :|  ::  | | || :|
Db      2006 TNPLMAVASPTEGV-----TATKGLVIQIISVLAIV-----GGCALGVKGI 2046

Qy      182 AD-----AKFRRVPRI LVCGRISLAKEVFGETL NESRDPDRAPER YTSR 225
      ||  | : : : | | |  || : |  : : | |
Db      2047 ADIWKISDDIKRGQATVFAYAQPIAMLA VAGGIIYLSTKFGFNIGEGGASVDQQQETKR 2106

Qy      226 FYLKFKHLERAFDMLSECGFHMVACNSSVTASFINQYTD DKIWSSYTEYVFY----- 277
      : :  | |  | |: | |  :  : |:  :: |:
Db      2107 LFFESSLKSRCFQ-----FVWVSKQRSQKRSTRKRKKHSQ-WACLYKFRFFQSDYQKFE 2159

Qy      278 REPSRWSPSHC-----DCCCKNGKG-----DKEGESGTSC--NDLSTSSCDS 317
      |: | : |  ||  ||  : :| :| |  | |:
Db      2160 RQESNFQRSQSRYYQRSFLRDCQSPKNKGFEALRSSYKNLKGNGIECRITDQSSERLFY 2219

Qy      318 QSEASSPQETVICGPVTRQTNIQTLDRPIKKGPVQLIQQSEM--RRKS--DLLRILTSG- 372
      :  |:| :  : |:  ::  | :| :  | || | :||  ||
Db      2220 FQKHQHDQQTLLSVIARRNKRNSMRVICFIGRIQFLSSFETYHRRVSQKNLLYDMSGI 2279

Qy      373 --SRESNMSSKKKAVKEKLSIEEELEK 397
      ||  ::||:  ::|| ||:|::|
Db      2280 SIKREVFVASKQADEQKKLIIEQEVQK 2306

```

RESULT 12

US-08-976-255-10
; Sequence 10, Application US/08976255
; Patent No. 6136581
; GENERAL INFORMATION:
; APPLICANT: Jono, Keith E.
; APPLICANT: Plowman, Gregory
; TITLE OF INVENTION: KINASE GENES AND USES
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,255
; FILING DATE: No. 6136581ember 21, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031,675
; FILING DATE: No. 6136581ember 22, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 229/182
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 848 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-976-255-10

Query Match 4.0%; Score 92.5; DB 3; Length 848;
Best Local Similarity 28.8%; Pred. No. 1.8;
Matches 40; Conservative 19; Mismatches 53; Indels 27; Gaps 6;

Qy 288 CDCCCKNGKGDKEGESGTSNDLSTSSCDSQSEASSPQETVICGPVTRQTNIQTLDLRPIK 347
| | | | | | | | | | | | | | | | | | : : |:
Db 61 CLCCKKGGIGFKEFE-----NAEGEYVADFSEQGSPAATVQNGPDVYVLPTEVSLPMA 115

Qy 348 KGP---VQLIQQSEMRRKSDLRI-----LTSGSRESNMSSKKKAVKE---KLSI 391
| | | | | : : : | | | : : | | : | | : | | | |:
Db 116 KQPGRSVQLLKSTD LGRHS-LLYLKEIGHGWFGKVFLGEVHSGVSGTQVVVKELKASASV 174

Qy 392 EEELEKCIQDFLKKKIPDR 410
:|::: ||:: | |
Db 175 QEQQM-----FLEEAQPYR 188

RESULT 13

US-09-252-991A-25633
; Sequence 25633, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25633
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25633

Query Match 4.0%; Score 92; DB 4; Length 393;
Best Local Similarity 22.4%; Pred. No. 0.64;
Matches 44; Conservative 20; Mismatches 76; Indels 56; Gaps 7;

Qy 234 ERAFDMLSECGFHMVA-CNSSVTASFINQYTDCKIWSSYTEYVFYREPSRWSPSHCDCC- 291
|| || |: | || | | || : ||
Db 3 ERCRKNCCACGKRCVSPCCSSPTPS-----RRRWWWATASCCS 40

Qy 292 --CKNGKGDKEGESGTSCNDLSTSSCDSQSEASSPQETVICGPVTRQTNIQTLDRPIKKG 349
: | | | : : | |: | | : : || | | || |
Db 41 RRTRGGSGPKCTATRSGCTALAASRCKPRRDAS----TACCS--TRAAN----- 83

Qy 350 PVQLIQQSEMRRKSDLLRILTSRSGSRESNMSSKKKAVKEKLSIEEELEKCIQDFLKKKIPD 409
||: | || : : :: : || | :: | :
Db 84 -----RRRP---RPSTSPISGWPIEQNRMSRVTRVREEYEVQLEPLLEVSLER 130

Qy 410 RFPERKHPWQSELLRK 425
| | : || |||
Db 131 RLPLSQRLWQQGWLRLK 146

RESULT 14

US-09-142-791A-2
; Sequence 2, Application US/09142791A
; Patent No. 6368823
; GENERAL INFORMATION:
; APPLICANT: Antoine Michel Alain Brill
; APPLICANT: Thierry Paul Gerard Calmels

```
; APPLICANT: Jean-Francois Simon Pierre Faivre
; APPLICANT: Jean-Luc Javre
; APPLICANT: Sabine Rouanet
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30012
; CURRENT APPLICATION NUMBER: US/09/142,791A
; CURRENT FILING DATE: 1999-02-02
; PRIOR APPLICATION NUMBER: PCT/EP98/01901
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: UK 9706377.0
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: EP 97402971.2
; PRIOR FILING DATE: 1997-12-09
; PRIOR APPLICATION NUMBER: EP 97403007.4
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 636
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-142-791A-2
```

```
Query Match          4.0%; Score 92; DB 4; Length 636;
Best Local Similarity 24.1%; Pred. No. 1.3;
Matches 32; Conservative 26; Mismatches 43; Indels 32; Gaps 5;

Qy      25 EVVELNVGGQVYFTRHSTLISIPHSLLW---KMFSPKRDTANDLAKDSKGRFFIDRDGFL 81
      |:: ||| |: : | :|| | :|| | | | :| ||| :
Db      40 ELIVLNVSGRRFQTWRTTLERYPDTLLGSTKEFFFNEDTK-----EYFFDRDPEV 90

Qy      82 FRYILDYLRDRQVVLDPHFPEKGRLK----REAEYFQLPDLVKLLTPDEIKQSPDEFCHS 137
      || :|:: | :: | :| : | | ||:: : | :
Db      91 FRCVLNIFYRTGKL----HYPRYECISAYDDELA FYGILPEII-----GDCCYE 134

Qy      138 DFEDASQGS DTRI 150
      ::| : : | :
Db      135 EYKDRKRENAERL 147
```

RESULT 15

US-09-178-109-4

```
; Sequence 4, Application US/09178109
; Patent No. 6395477
; GENERAL INFORMATION:
; APPLICANT: Cockett, Mark I.
; APPLICANT: Dilks, Daniel W.
; APPLICANT: Chang Ling, Huai-Ping
; APPLICANT: Sokol, Patricia T.
; TITLE OF INVENTION: Human Potassium Channel Polynucleotides and
; TITLE OF INVENTION: Polypeptides and Uses Therefor
; FILE REFERENCE: ahp-98089
; CURRENT APPLICATION NUMBER: US/09/178,109
; CURRENT FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
```

; LENGTH: 636
; TYPE: PRT
; ORGANISM: human
US-09-178-109-4

Query Match 4.0%; Score 92; DB 4; Length 636;
Best Local Similarity 24.1%; Pred. No. 1.3;
Matches 32; Conservative 26; Mismatches 43; Indels 32; Gaps 5;

```
Qy      25 EVVELNVGGQVYFTRHSTLISIPHSLLW---KMFSPKRDTANDLAKDSKGRFFIDRDGFL 81
          |:: ||| |: : | :|| | :|| | | | :| ||| :
Db      40 ELIVLNVSGRRFQTWRTTLERYPDTLLGSTEKEFFFNEDTK-----EYFFDRDPEV 90

Qy      82 FRYILDYLRDRQVVLDPHFPEKGRLK----REAEYFQLPDLVKLLTPDEIKQSPDEFCHS 137
          || :|:: | :: | :| : | | ||:: : | :
Db      91 FRCVLNFYRTGKL----HYPRYECISAYDDELA FYGILPEII-----GDCCYE 134

Qy      138 DFEDASQGS DTRI 150
          :::| : : | :
Db      135 EYKDRKRENAERL 147
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Search completed: January 29, 2004, 02:56:18
Job time : 25 secs

OM protein - protein search, using sw model

Run on: January 29, 2004, 02:52:31 ; Search time 306 Seconds
(without alignments)
289.161 Million cell updates/sec

Title: US-10-056-884A-2
Perfect score: 2284
Sequence: 1 MALSGNCSRYYPREQGSAVP.....DRFPERKHPWQSELLRKYHL 428

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 777136 seqs, 206736638 residues

Total number of hits satisfying chosen parameters: 777136

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	
No.	Score Match Length DB ID	Description

1	2284	100.0	428	15	US-10-056-884-2	Sequence 2, Appli
2	2271	99.4	435	15	US-10-080-980-4	Sequence 4, Appli
3	832	36.4	325	15	US-10-080-980-2	Sequence 2, Appli
4	541	23.7	103	15	US-10-056-884-20	Sequence 20, Appl
5	538.5	23.6	228	15	US-10-056-884-5	Sequence 5, Appli
6	538.5	23.6	228	15	US-10-080-980-3	Sequence 3, Appli
7	367	16.1	101	15	US-10-080-980-13	Sequence 13, Appl
8	345.5	15.1	190	15	US-10-056-884-6	Sequence 6, Appli
9	234.5	10.3	351	15	US-10-086-156-2	Sequence 2, Appli
10	226	9.9	99	15	US-10-086-156-12	Sequence 12, Appl
11	210	9.2	256	12	US-10-234-951A-4	Sequence 4, Appli
12	210	9.2	256	15	US-10-056-884-7	Sequence 7, Appli
13	210	9.2	256	15	US-10-080-980-6	Sequence 6, Appli
14	210	9.2	256	15	US-10-121-746-14	Sequence 14, Appl
15	210	9.2	256	15	US-10-086-156-4	Sequence 4, Appli
16	210	9.2	257	12	US-10-234-951A-6	Sequence 6, Appli
17	210	9.2	257	15	US-10-192-116A-6	Sequence 6, Appli
18	210	9.2	257	15	US-10-071-458-3	Sequence 3, Appli
19	204	8.9	213	12	US-10-168-651-11	Sequence 11, Appl
20	204	8.9	213	14	US-10-024-579-2	Sequence 2, Appli
21	203	8.9	528	15	US-10-192-116A-2	Sequence 2, Appli
22	202.5	8.9	237	12	US-10-234-951A-3	Sequence 3, Appli
23	202.5	8.9	237	12	US-10-264-171-3	Sequence 3, Appli
24	202.5	8.9	237	15	US-10-040-805-3	Sequence 3, Appli
25	202.5	8.9	237	15	US-10-056-884-4	Sequence 4, Appli
26	202.5	8.9	237	15	US-10-080-980-7	Sequence 7, Appli
27	202.5	8.9	237	15	US-10-080-980-9	Sequence 9, Appli
28	202.5	8.9	237	15	US-10-121-746-25	Sequence 25, Appl
29	202.5	8.9	237	15	US-10-086-156-3	Sequence 3, Appli
30	202.5	8.9	237	15	US-10-071-458-6	Sequence 6, Appli
31	201.5	8.8	257	14	US-10-024-579-14	Sequence 14, Appl
32	201.5	8.8	283	14	US-10-024-579-10	Sequence 10, Appl
33	193.5	8.5	140	15	US-10-080-980-5	Sequence 5, Appli
34	191	8.4	75	12	US-09-864-408A-7362	Sequence 7362, Ap
35	189	8.3	225	15	US-10-086-156-25	Sequence 25, Appl
36	189	8.3	255	12	US-10-168-651-4	Sequence 4, Appli
37	189	8.3	255	12	US-10-264-171-2	Sequence 2, Appli
38	189	8.3	255	15	US-10-040-805-2	Sequence 2, Appli
39	189	8.3	258	12	US-10-234-951A-5	Sequence 5, Appli
40	189	8.3	258	15	US-10-121-746-12	Sequence 12, Appl
41	185	8.1	197	15	US-10-106-698-4675	Sequence 4675, Ap
42	184	8.1	175	9	US-09-925-299-879	Sequence 879, App
43	184	8.1	175	11	US-09-925-299-879	Sequence 879, App
44	174.5	7.6	238	14	US-10-024-579-16	Sequence 16, Appl
45	174.5	7.6	264	14	US-10-024-579-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
 US-10-056-884-2
 ; Sequence 2, Application US/10056884
 ; Publication No. US20030032786A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company


```
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL
BETA-SUBUNIT,
; TITLE OF INVENTION: K+betaM2
; FILE REFERENCE: D0076 NP
; CURRENT APPLICATION NUMBER: US/10/056,884
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US 60/263,872
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: US 60/269,794
; PRIOR FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-056-884-2
```

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Query Match          100.0%;  Score 2284;  DB 15;  Length 428;
Best Local Similarity 100.0%;  Pred. No. 6.7e-215;
Matches 428;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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Qy      1 MALSGNCSRYYPREQGSAVPNSFPEVVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRD 60
        |||
Db      1 MALSGNCSRYYPREQGSAVPNSFPEVVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRD 60

Qy     61 TANDLAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLDPHFPEKGRLKREAEYFQLPDLVK 120
        |||
Db     61 TANDLAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLDPHFPEKGRLKREAEYFQLPDLVK 120

Qy    121 LLTPDEIKQSPDEFCHSDFEDASQGS DTRICPPSSLLPADRKWGFITVGYRGSC TLGREG 180
        |||
Db    121 LLTPDEIKQSPDEFCHSDFEDASQGS DTRICPPSSLLPADRKWGFITVGYRGSC TLGREG 180

Qy    181 QADAKFRRVPRI LVCGRISLAKEVFGETL NESRDPDRAPER YTSRFY LKFKHLERA F DML 240
        |||
Db    181 QADAKFRRVPRI LVCGRISLAKEVFGETL NESRDPDRAPER YTSRFY LKFKHLERA F DML 240

Qy    241 SEC GFH MVACN SSVTASFINQY TDDKI WSSY TEYVFY REPSRWSP SHC DCCCKNGKGDKE 300
        |||
Db    241 SEC GFH MVACN SSVTASFINQY TDDKI WSSY TEYVFY REPSRWSP SHC DCCCKNGKGDKE 300

Qy    301 GESGTSCNDLSTSSCDSQSEASSPQETVICGPVTRQTNIQT LDRPIKKG PVQLIQQSEMR 360
        |||
Db    301 GESGTSCNDLSTSSCDSQSEASSPQETVICGPVTRQTNIQT LDRPIKKG PVQLIQQSEMR 360

Qy    361 RKSDLLRILTSGSRESNMSSKKKAVKEKLSIEEELEKCIQDFLKKKIPDRFPERKHPWQS 420
        |||
Db    361 RKSDLLRILTSGSRESNMSSKKKAVKEKLSIEEELEKCIQDFLKKKIPDRFPERKHPWQS 420

Qy    421 ELLRKYHL 428
        |||
Db    421 ELLRKYHL 428
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```
RESULT 2
US-10-080-980-4
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; Sequence 4, Application US/10080980
; Publication No. US20030036115A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL
BETA-SUBUNIT,
; TITLE OF INVENTION: K+betaM6, EXPRESSED HIGHLY IN THE SMALL INTESTINE
; FILE REFERENCE: D0121 NP
; CURRENT APPLICATION NUMBER: US/10/080,980
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/270,132
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 60/278,953
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-080-980-4
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Query Match          99.4%; Score 2271; DB 15; Length 435;
Best Local Similarity 99.5%; Pred. No. 1.3e-213;
Matches 426; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy      1 MALSGNCSRYYPREQGSAVPNSFPEVVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRD 60
      |||
Db      8 MALSGNCSRYYPREQGSAVPNSFPEVVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRD 67

Qy     61 TANDLAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLDPDHFPEKGRLKREAEYFQLPDLVK 120
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Db     68 TANDLAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLDPDHFPEKGRLKREAEYFQLPDLVK 127

Qy    121 LLTPDEIKQSPDEFCHSDFEDASQGS DTRICPPSSLLPADRKWGFITVGYRGSC T L GREG 180
      |||
Db    128 LLTPDEIKQSPDEFCHSDFEDASQGS DTRICPPSSLLPADRKWGFITVGYRGSC T L GREG 187

Qy    181 QADAKFRRVPRI LVCGRISLAKEVFGETL NESRDPDRAPER YTSRFY LKF KHLERA F DML 240
      |||
Db    188 QADAKFRRVPRI LVCGRISLAKEVFGETL NESRDPDRAPER YTSRFY LKF KHLERA F DML 247

Qy    241 SEC GFH MVACN SSVTASFINQYTD D KIWSSYTEYVFYREPSRWSPSHCDCCCKNGKGDKE 300
      |||
Db    248 SEC GFH MVACN SSVTASFINQYTD D KIWSSYTEYVFYREPSRWSPSHCDCCCKNGKGDKE 307

Qy    301 GESGTSCNDLSTSSCDSQSEASSPQETVICGPVTRQTNIQTLD RPIKKG P VQLIQQSEMR 360
      |||
Db    308 GESGTSCNDLSTSSCDSQSEASSPQETVICGPVTRQTNIQTLD RPIKKG P VQLIQQSEMR 367

Qy    361 RKSDLLRILTSGSRESNMSSKKKAVKEKLSIEEELEKCIQDFLKKKI PDRFPERKHPWQS 420
      |||
Db    368 RKSDLLRTLTSGSRESNMSSKKKAVKEKLSIEEELEKCIQDFLKKKI PDRFPERKHPWQS 427

Qy    421 ELLRKYHL 428
      |||
Db    428 ELLRKYHL 435
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RESULT 3

US-10-080-980-2

; Sequence 2, Application US/10080980
 ; Publication No. US20030036115A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL
 BETA-SUBUNIT,
 ; TITLE OF INVENTION: K+betaM6, EXPRESSED HIGHLY IN THE SMALL INTESTINE
 ; FILE REFERENCE: D0121 NP
 ; CURRENT APPLICATION NUMBER: US/10/080,980
 ; CURRENT FILING DATE: 2002-02-21
 ; PRIOR APPLICATION NUMBER: US 60/270,132
 ; PRIOR FILING DATE: 2001-02-21
 ; PRIOR APPLICATION NUMBER: US 60/278,953
 ; PRIOR FILING DATE: 2001-03-27
 ; NUMBER OF SEQ ID NOS: 74
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 325
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-080-980-2

Query Match 36.4%; Score 832; DB 15; Length 325;
 Best Local Similarity 54.0%; Pred. No. 8.6e-73;
 Matches 170; Conservative 41; Mismatches 56; Indels 48; Gaps 6;

Qy	4	SGNCSRYYPREQGSAVPNSFPEVVELNVGGQVYFTRHSTLISIPHSLWKMFSKPRDTAN	63
		: :: ::: : : ::	
Db	20	SGSSS-----SSAEPPLFPDIVELNVGGQVYVTRRCTVVSVPDSSLWRMFTQQQ--PQ	70
Qy	64	DLAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLDPHFPEKGRKREAEYFQLPDLVKLL-	122
		: : : :: : : : : :	
Db	71	ELARDSKGRFFLDRDGLFRYILDYLRDLQLVLPDYFPERSRLQREAEYFELPELVRRLG	130
Qy	123	TPDEIKQSP-----DEFCHSDFEDASQ-----GS	146
		: : : :	
Db	131	APQQPGPGPPPSRRGVHKEGSLGDELLPLGYSEPEQQEGASAGAPSPITLELASRSPSGGA	190
Qy	147	DTRICPPSSLLPADRKWGFITVGYRGSCTLGREGQADAKFRRVPRIILVCGRISLAKEVFG	206
		: : : : : : :	
Db	191	AGPLLTPSQSLDGSRSGYITIGYRGSYTIGRDAQADAKFRRVARITVCGKTSLAKEVFG	250
Qy	207	ETLNESRDPDRAPERYTSRFYLFKHLERAFDMLSECGFHMVACNSSVTASFIN--QYTD	264
		: : : : : : : ::	
Db	251	DTLNESRDPDRPPERYTSRYLLKFNFLQAFDKLSESGFHMVACSSGTGCAFASSTDQSE	310
Qy	265	DKIWSSYTEYVFYRE	279
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Db	311	DKIWTSYTEYVFCRE	325

RESULT 4

US-10-056-884-20

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; Sequence 20, Application US/10056884
; Publication No. US20030032786A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL
BETA-SUBUNIT,
; TITLE OF INVENTION: K+betaM2
; FILE REFERENCE: D0076 NP
; CURRENT APPLICATION NUMBER: US/10/056,884
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US 60/263,872
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: US 60/269,794
; PRIOR FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-056-884-20
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Query Match          23.7%; Score 541; DB 15; Length 103;
Best Local Similarity 100.0%; Pred. No. 5.1e-45;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      25 EVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFLFRY 84
          |||
Db      1 EVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFLFRY 60

Qy      85 ILDYLRDRQVVLDPDHFPEKGRLKREAEIFQLPDLVKLLTPDEI 127
          |||
Db      61 ILDYLRDRQVVLDPDHFPEKGRLKREAEIFQLPDLVKLLTPDEI 103
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RESULT 5

US-10-056-884-5

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; Sequence 5, Application US/10056884
; Publication No. US20030032786A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL
BETA-SUBUNIT,
; TITLE OF INVENTION: K+betaM2
; FILE REFERENCE: D0076 NP
; CURRENT APPLICATION NUMBER: US/10/056,884
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US 60/263,872
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: US 60/269,794
; PRIOR FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
```

US-10-056-884-5

Query Match 23.6%; Score 538.5; DB 15; Length 228;
Best Local Similarity 44.3%; Pred. No. 2.9e-44;
Matches 116; Conservative 44; Mismatches 61; Indels 41; Gaps 7;

```
Qy      24 PEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSKRDANDLAKDSKGRFFIDRDGFLFR 83
      ||::||||| | | :||:  :|| ::|  ||:  ||| |||::|:|||| |||
Db      2 PEIIELVGGVSYTTTLATLLQDKSTLLAELFGEGRDS---LAKDSKGRYFLDRDGVFLFR 58

Qy      84 YILDYLRDRQVVLDPHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQSPDEFCHSDFEDAS 143
      |||::|||: : ||: | |: || |||::|:| ::: : :
Db      59 YILDFLRDKALHLEPGFRERQRLLEAEHFKLTAMLECI RSE R----- 101

Qy     144 QGSDTRICPPSSLLPADRKWGFITVGYRGSCITLGREGQADAKFRRVPRILVCGRISLAKE 203
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     102 ---DAR--PP-----GCITIGYRGSFQFGKDLADVKFRKLSRILVCGRVAQCRE 146

Qy     204 VFGETLINESRDPDR-APERYTSRFYLFKHLERAFDMLSECGFHMV-ACNSSVTASFINQ 261
      |||:||||||| | :|||::| | :|:| | | : | : | : | | |
Db     147 VFGDTLINESRDPDHGGTDRTYTSRFFLKHCYIEQAFDNLHDHGYRMAGSCGSGTAGSAAEP 206

Qy     262 Y----TDDKIWSSYTEYVFYRE 279
      |:: | : | | :| | | :
Db     207 KPGVDTEENRWNHYNEFVFIRD 228
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RESULT 6

US-10-080-980-3

; Sequence 3, Application US/10080980
; Publication No. US20030036115A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL BETA-SUBUNIT,
; TITLE OF INVENTION: K+betaM6, EXPRESSED HIGHLY IN THE SMALL INTESTINE
; FILE REFERENCE: D0121 NP
; CURRENT APPLICATION NUMBER: US/10/080,980
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/270,132
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 60/278,953
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-080-980-3

Query Match 23.6%; Score 538.5; DB 15; Length 228;
Best Local Similarity 44.3%; Pred. No. 2.9e-44;
Matches 116; Conservative 44; Mismatches 61; Indels 41; Gaps 7;

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Qy      24 PEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSKRDANDLAKDSKGRFFIDRDGFLFR 83
      ||::||||| | | :||:  :|| ::|  ||:  ||| |||::|:|||| |||
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US-10-056-884-6
; Sequence 6, Application US/10056884
; Publication No. US20030032786A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL BETA-SUBUNIT,
; TITLE OF INVENTION: K+betaM2
; FILE REFERENCE: D0076 NP
; CURRENT APPLICATION NUMBER: US/10/056,884
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US 60/263,872
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: US 60/269,794
; PRIOR FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-056-884-6

Query Match 15.1%; Score 345.5; DB 15; Length 190;
Best Local Similarity 39.6%; Pred. No. 1.8e-25;
Matches 80; Conservative 34; Mismatches 59; Indels 29; Gaps 4;

Qy 22 SFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSK-----GRF 73
| :|: ||||| :| | ||| :|| :| |::| : |
Db 3 SVEDVITLNVGGTMYTTTRSTLSKETDTLLANIAS-----GSLSEDEQANVVTLPDGT 56
Qy 74 FIDRDGFLFRYILDYLRDRQVVLDPHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQSPDE 133
|:|||| || |:| :|| :: ||: | | ||| ||:::| ||: : ||
Db 57 FVDRDGPLFAYVLHFLRTDKLSLPEQFREVARLKDEADFYRLERFSTLLS-NASSISPRP 115
Qy 134 FCHSDFEDASQGS DTRICPPSSLLPADRKWGFITVGYRGSC TLGREGQADAKFRRVPRIL 193
: : : |::| |::| |||: ||: ||| |||:: |||
Db 116 RTANGYNTITSGAET-----GGYITLGYRGTF AFGRDGGQADVKFRKLHRI 161
Qy 194 VCGRISLAKEVFGETL NESRDP 215
|||| :| :||| :|||||||
Db 162 VCGRATLCREVFADT LNESRDP 183

RESULT 9

US-10-086-156-2
; Sequence 2, Application US/10086156
; Publication No. US20030054989A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING TWO NOVEL HUMAN POTASSIUM CHANNEL BETA-SUBUNITS,
; TITLE OF INVENTION: K+betaM4 and K+betaM5
; FILE REFERENCE: D0115NP
; CURRENT APPLICATION NUMBER: US/10/086,156
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/272,190

; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/274,258
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 351
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-086-156-2

Query Match 10.3%; Score 234.5; DB 15; Length 351;
Best Local Similarity 40.3%; Pred. No. 3.4e-14;
Matches 52; Conservative 26; Mismatches 44; Indels 7; Gaps 2;

Qy 8 SRYYPREQGSAVPNSFP---EVVELNVGGQVYFTRHSTLISIPHSLLWKMFSKRDAND 64
:|:: :| : : |||||::| :|| | | :| || | |
Db 74 TRFFSCREGLLPATQSPAMSDPITLVNKGKLYTTSLATLTSFPDSMLGAMFSGKMPT--- 130

Qy 65 LAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLDPHFPEKGRLLKREAEYFQLPDLVKLLTP 124
:||:| ||||| :|||||::|| : ||: | | | |:|||:::|: |:: |
Db 131 -KRDSQGNCFIDRDGKVFRIYILNFLRTSHLDLPEDFQEMGLLRREADFYQVQPLIEALQE 189

Qy 125 DEIKQSPDE 133
|:: | |
Db 190 KEVELSKAE 198

RESULT 10

US-10-086-156-12

; Sequence 12, Application US/10086156
; Publication No. US20030054989A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING TWO NOVEL HUMAN POTASSIUM CHANNEL
BETA-SUBUNITS,
; TITLE OF INVENTION: K+betaM4 and K+betaM5
; FILE REFERENCE: D0115NP
; CURRENT APPLICATION NUMBER: US/10/086,156
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/272,190
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/274,258
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 99
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-086-156-12

Query Match 9.9%; Score 226; DB 15; Length 99;
Best Local Similarity 46.5%; Pred. No. 3.6e-14;
Matches 47; Conservative 20; Mismatches 30; Indels 4; Gaps 1;

Qy 27 VELNVGGQVYFTRHSTLISIPHSLLWKMFSKRDANDLAKDSKGRFFIDRDGFLFRYIL 86


```

      : |||||::| | :|| | | |:| ||| | | :||:| ||||| :||||
Db      3 ITLNVGGKLYTTSLATLTSPDMLGAMFSGKMPT-----KRDSQGNCFIDRDGKVFRYIL 58

Qy      87 DYLRDRQVVLPDHFPEKGRLLKREAEYFQLPDLVKLLTPDEI 127
      ::|| : ||: | | | |:||||::|: |:: | |:
Db      59 NFLRTSHLDLPEDFQEMGLLRREADFYQVQPLIEALQEKEV 99

```

RESULT 11

US-10-234-951A-4

```

; Sequence 4, Application US/10234951A
; Publication No. US20030162251A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL
; TITLE OF INVENTION: BETA-SUBUNIT, K+betaM8
; FILE REFERENCE: D0162 NP
; CURRENT APPLICATION NUMBER: US/10/234,951A
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: U.S. 60/317,087
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: U.S. 60/329,666
; PRIOR FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (15)..(15)
; OTHER INFORMATION: wherein "X" equals any amino acid.
US-10-234-951A-4

```

```

Query Match          9.2%; Score 210; DB 12; Length 256;
Best Local Similarity 28.7%; Pred. No. 5.4e-12;
Matches 77; Conservative 39; Mismatches 82; Indels 70; Gaps 12;

```

```

Qy      27 VELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDS-KGRFFIDRDGFLFRYI 85
      | ::||| :| : :|| | | :::| | : || | :||||| :||||
Db      32 VHIDVGGHMYTSSLATLTYPESRIGRLF-----DGTEPIVLDSLKQHYFIDRDGQMFYI 87

Qy      86 LDYLRDRQVVLPDHFPEKGRLLKREAEYFQLPDLVKLLTPDEIKQSPDEFCHSDFEDASQG 145
      |::|| ::::|| | : | ||:|||| : || : || | |
Db      88 LNFLRTSKLLIPDDFKDYTLLEYEAKYFQLQPM--LLEMERWKQ-----DRETG 134

Qy      146 SDTRICPPSSLLPADRKWGFITVGYRGSCITLGREGQADAKFRRVPRIIVCGRISLAKEVF 205
      :| | : | : || | | : | || :|||
Db      135 RFSRPCE-----CLVVRVAPDLGE-----RITLSGDKSLIEEVF 168

Qy      206 GE-----TLNESRDPDRAPERYTSRFYLYK-FKHLE--RAFDMLSECGFHMV-ACNSSV 254
      | :|| : | : || | : || : : | : || :| :| |
Db      169 PEIGDVMCNSVNAGWNHD---STHVIRFPLNGYCHLNSVQVLERLQQRGFEIVGSCGGGV 225

Qy      255 TASFINQYTDCKIWSSYTEYVFYREPSR 282
      : | ::||| || |

```

Db 226 DS-----SQFSEYVLRRELRR 241

RESULT 12

US-10-056-884-7

; Sequence 7, Application US/10056884

; Publication No. US20030032786A1

; GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company

; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL BETA-SUBUNIT,

; TITLE OF INVENTION: K+betaM2

; FILE REFERENCE: D0076 NP

; CURRENT APPLICATION NUMBER: US/10/056,884

; CURRENT FILING DATE: 2002-01-24

; PRIOR APPLICATION NUMBER: US 60/263,872

; PRIOR FILING DATE: 2001-01-24

; PRIOR APPLICATION NUMBER: US 60/269,794

; PRIOR FILING DATE: 2001-02-14

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 7

; LENGTH: 256

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: variant

; LOCATION: (15)..(15)

; OTHER INFORMATION: wherein "Xaa" is unknown.

US-10-056-884-7

Query Match 9.2%; Score 210; DB 15; Length 256;

Best Local Similarity 28.7%; Pred. No. 5.4e-12;

Matches 77; Conservative 39; Mismatches 82; Indels 70; Gaps 12;

Qy 27 VELNVGGQVYFTRHSTLISIPHSLLWKMFSKPRDTANDLAKDS-KGRFFIDRDGFLFRYI 85

| ::||| :| : :|| | | : ::| | : || | :||| | :|||

Db 32 VHIDVGGHMYTSSLATLTYPESRIGRLF----DGTEPIVLDSLKQHYFIDRDGQMFYI 87

Qy 86 LDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQSPDEFCHSDFEDASQG 145

| ::|| : ::|| | : | ||:|||| : || : || | |

Db 88 LNFLRTSKLLIPDDFKDYTLLEYEAKYFQLQPM--LLEMERWKQ-----DRETG 134

Qy 146 SDTRICPPSSLLPADRKWGFITVGYRGSGCTLGREGQADAKFRRVPRILVCGRISLAKEVF 205

:| | : | : || || : | || :|||

Db 135 RFSRPCE-----CLVVRVAPDLGE-----RITLSGDKSLIEEVF 168

Qy 206 GE-----TLNESRDPDRAPERYTSRFYLK-FKHLE--RAFDMLSECGFHMV-ACNSSV 254

| :| : | : || | : || : : | : || :| :|

Db 169 PEIGDVMCNSVNAGWNHD---STHVIRFPLNGYCHLNSVQVLERLQQRGFIEVGSCGGGV 225

Qy 255 TASFINQYTDDKIWSSYTEYVFYREPSR 282

: | :||| || |

Db 226 DS-----SQFSEYVLRRELRR 241

RESULT 13

US-10-080-980-6
; Sequence 6, Application US/10080980
; Publication No. US20030036115A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL
BETA-SUBUNIT,
; TITLE OF INVENTION: K+betaM6, EXPRESSED HIGHLY IN THE SMALL INTESTINE
; FILE REFERENCE: D0121 NP
; CURRENT APPLICATION NUMBER: US/10/080,980
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/270,132
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 60/278,953
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (15)..(15)
; OTHER INFORMATION: wherein "X" is equal to any amino acid.
US-10-080-980-6

Query Match 9.2%; Score 210; DB 15; Length 256;
Best Local Similarity 28.7%; Pred. No. 5.4e-12;
Matches 77; Conservative 39; Mismatches 82; Indels 70; Gaps 12;

Qy 27 VELNVGGQVYFTRHSTLISIPHSLLWKMFSKPRDTANDLAKDS-KGRFFIDRDGFLFRYI 85
| :||| :| : :|| | | : :| | : || | :||| :|||
Db 32 VHIDVGGHMYTSSLATLTYPESRIGRLF----DGTEPIVLDSLKQHYFIDRDGQMFYI 87
Qy 86 LDYLRDRQVVLDPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQSPDEFCHSDFEDASQG 145
| :||| :||| | : | ||| : || : || | |
Db 88 LNFLRTSKLLIPDDFDKYTLLEYEAKYFQLQPM--LLEMERWKQ-----DRETG 134
Qy 146 SDTRICPPSSLLPADRKWGFITVGYRGSGTLGREGQADAKFRRVPRILVCGRISLAKEVE 205
:| | : | : || || : | |||
Db 135 RFSRPCE-----CLVVRVAPDLGE-----RITLSGDKSLIEEVF 168
Qy 206 GE-----TLNESRDPDRAPERYTSRFYLYK-FKHLE--RAFDMLSECGFHMV-ACNSSV 254
| :|| :| : ||| : || : : | : || :| :|
Db 169 PEIGDVMCNSVNAGWNHD---STHVIRFPLNGYCHLNSVQVLERLQQRGFEIVGSCGGGV 225
Qy 255 TASFINQYTDDKIWSSYTEYVFYREPSR 282
: | :||| || |
Db 226 DS-----SQFSEYVLRRELRR 241

RESULT 14

US-10-121-746-14
; Sequence 14, Application US/10121746
; Publication No. US20030036648A1
; GENERAL INFORMATION:

```
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. US20030036648A1e1 Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/10/121,746
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US/09/336,643A
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 256
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(256)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-121-746-14
```

```
Query Match          9.2%; Score 210; DB 15; Length 256;
Best Local Similarity 28.7%; Pred. No. 5.4e-12;
Matches 77; Conservative 39; Mismatches 82; Indels 70; Gaps 12;
```

```
Qy      27 VELNVGGQVYFTRHSTLISIPHSLLWKMFSKPRDTANDLAKDS-KGRFFIDRDGFLFRYI 85
      |::||| :| : :|| | | : ::| | : || | :||| | :|||
Db      32 VHIDVGGHMYTSSLATLTYPESRIGRLF----DGTEPIVLDSLKQHYFIDRDGQMFYI 87

Qy      86 LDYLRDRQVVLDPHFPEKGRLEAEYFQLPDLVKLLTPDEIKQSPDEFCHSDFEDASQG 145
      |::|| ::::| | : | ||:| | : || : || | | |
Db      88 LNFLRTSKLLIPDDFKDYTLLEYEAKYFQLQPM--LLEMERWKQ-----DRETG 134

Qy     146 SDTRICPPSSLLPADRKWGFITVGYRGSCITLGREGQADAKFRRVPRILVCGRISLAKEVF 205
      :| | : | : | | | | | | | | | | | | | | | |
Db     135 RFSRPE-----CLVVRVAPDLGE-----RITLSGDKSLIEEVF 168

Qy     206 GE-----TLNESRDPDRAPERYTSRFYLYK-FKHLE--RAFDMLSECGFHMV-ACNSSV 254
      | : : | : | : || | : || : : | : || : | : |
Db     169 PEIGDVMCNSVNAGWNHD---STHVIRFPLNGYCHLNSVQVLERLQQRGFIVGSCGGGV 225

Qy     255 TASFINQYTDCKIWSSYTEYVFYREPSR 282
      : | :||| || |
Db     226 DS-----SQFSEYVLRRELRR 241
```

```
RESULT 15
US-10-086-156-4
; Sequence 4, Application US/10086156
```

```

; Publication No. US20030054989A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING TWO NOVEL HUMAN POTASSIUM CHANNEL
BETA-SUBUNITS,
; TITLE OF INVENTION: K+betaM4 and K+betaM5
; FILE REFERENCE: D0115NP
; CURRENT APPLICATION NUMBER: US/10/086,156
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/272,190
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/274,258
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 256
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (15)..(15)
; OTHER INFORMATION: wherein "X" is equal to any amino acid.
US-10-086-156-4

```

```

Query Match          9.2%; Score 210; DB 15; Length 256;
Best Local Similarity 28.7%; Pred. No. 5.4e-12;
Matches 77; Conservative 39; Mismatches 82; Indels 70; Gaps 12;

```

```

Qy      27 VELNVGGQVYFTRHSTLISIPHSLWKMFS PKRDTANDLAKDS-KGRFFIDRDGFLFRYI 85
      |::||| :| : :|| | | : ::| | : || | :||| | :|||
Db      32 VHIDVGGHMYTSSLATLT KYPESRIGRLF----DGTEPIVLDSLKQHYFIDRDGQMFYI 87

Qy      86 LDYLRDRQVVLDPDHFPEKGR LKREAEYFQLPDLVKLLTPDEIKQSPDEFCHSD FEDASQG 145
      |::|| : ::|| | : | ||: ||| : || : || | |
Db      88 LNFLRTSKLLIPDDFKDY TLLYEEAKYFQLQPM--LLEMERWKQ-----DRETG 134

Qy      146 SDTRICPPSSLLPADRKWGFITVGYRG SCTLGREGQADAKFRRVPRI LVCGRISLAKEVF 205
      :| | : | : || | : | || :|||
Db      135 RFSRPCE-----CLVVRVAPDLGE-----RITLSGDKSLIEEVF 168

Qy      206 GE-----TLNESRDPDRAPER YTSRFY LK-FKHLE--RAFDMLSECGFHMV-ACNSSV 254
      | : :| : | : || | : || : : | : || :| :|
Db      169 PEIGDVMCNSVNAGWNHD---STHVIRFPLNGYCHLNSVQVLERLQQRGFEIVGSCGGGV 225

Qy      255 TASFINQYTDDKIWSSSYTEYVFYREPSR 282
      : : :||| || |
Db      226 DS-----SQFSEYVLRRELRR 241

```

```

Search completed: January 29, 2004, 03:01:31
Job time : 307 secs

```

OM protein - protein search, using sw model

Run on: January 29, 2004, 02:33:16 ; Search time 28 Seconds
(without alignments)
1470.007 Million cell updates/sec

Title: US-10-056-884A-2
Perfect score: 2284
Sequence: 1 MALSGNCSRYYPREQGSAVP.....DRFPERKHPWQSELLRKYHL 428

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	345.5	15.1	190	2	T26019	hypothetical prote
2	169.5	7.4	207	2	T31996	hypothetical prote
3	158.5	6.9	272	2	T15820	hypothetical prote
4	158	6.9	670	2	T32221	hypothetical prote
5	156	6.8	220	2	T20366	hypothetical prote
6	146.5	6.4	220	2	T33592	hypothetical prote
7	146	6.4	348	2	A41784	tumor necrosis fac
8	145.5	6.4	179	2	T33590	hypothetical prote
9	144	6.3	212	2	T31997	hypothetical prote
10	131.5	5.8	373	2	T26685	hypothetical prote
11	122.5	5.4	231	2	T32070	hypothetical prote
12	122.5	5.4	236	2	T33589	hypothetical prote
13	121.5	5.3	246	2	T25978	hypothetical prote

14	119	5.2	277	2	T21630	hypothetical prote
15	115.5	5.1	134	2	T32065	hypothetical prote
16	115	5.0	204	2	T25972	hypothetical prote
17	115	5.0	244	2	T25970	hypothetical prote
18	115	5.0	347	2	T31922	hypothetical prote
19	114.5	5.0	208	2	T25973	hypothetical prote
20	114	5.0	155	2	T25980	hypothetical prote
21	113.5	5.0	140	2	T25976	hypothetical prote
22	111	4.9	155	2	T25979	hypothetical prote
23	105	4.6	139	2	T32068	hypothetical prote
24	105	4.6	441	2	C84634	hypothetical prote
25	105	4.6	1504	2	A33602	DNA-directed DNA p
26	104.5	4.6	1176	2	A49848	nitrite reductase
27	104	4.6	108	2	T22320	hypothetical prote
28	104	4.6	294	2	T33588	hypothetical prote
29	104	4.6	490	2	A35312	potassium channel
30	104	4.6	491	2	JE0276	voltage-gated pota
31	103.5	4.5	84	2	T25977	hypothetical prote
32	103.5	4.5	140	2	A88479	protein F47D12.3 [
33	103	4.5	139	2	T25974	hypothetical prote
34	102	4.5	326	2	T32067	hypothetical prote
35	101.5	4.4	1537	2	JC4172	DNA (cytosine-5-)-
36	100.5	4.4	651	2	A39372	potassium channel
37	100	4.4	265	2	T32015	hypothetical prote
38	100	4.4	737	2	S18207	adducin alpha chai
39	99	4.3	232	2	D88076	protein K02F6.8 [i
40	98.5	4.3	745	2	T39952	hypothetical prote
41	98	4.3	329	2	A31595	interferon regulat
42	98	4.3	825	2	S26706	transcription fact
43	97.5	4.3	1213	2	A41724	limb deformity (ld
44	97	4.2	441	2	C85362	hypothetical prote
45	96.5	4.2	784	2	D96564	myosin-like protei

ALIGNMENTS

RESULT 1

T26019

hypothetical protein VM106R.1 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T26019

R;Barlow, K.

submitted to the EMBL Data Library, August 1998

A;Reference number: Z20135

A;Accession: T26019

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-190 <WIL>

A;Cross-references: EMBL:AL031266; PIDN:CAA20329.1; GSPDB:GN00020; CESP:VM106R.1

A;Experimental source: clone VM106R

C;Genetics:

A;Gene: CESP:VM106R.1

A;Map position: 2

A;Introns: 131/1

Query Match 15.1%; Score 345.5; DB 2; Length 190;
Best Local Similarity 39.6%; Pred. No. 8.5e-21;
Matches 80; Conservative 34; Mismatches 59; Indels 29; Gaps 4;

RESULT 2

hypothetical protein B0281.5 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jul-2000
C;Accession: T31996
R;Pauley, A.; Scheet, P.
submitted to the EMBL Data Library, July 1997
A;Description: The sequence of *C. elegans* cosmid B0281.
A;Reference number: Z21109
A;Accession: T31996
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-207 <PAU>
A;Cross-references: EMBL:AF016666; PIDN:AAB66084.1; GSPDB:GN00020; CESP:B0281.5
A;Experimental source: strain Bristol N2; clone B0281
C;Genetics:
A;Gene: CESP:B0281.5
A;Map position: 2
A;Introns: 38/3; 120/3; 160/1
C;Superfamily: *Caenorhabditis elegans* hypothetical protein ZC239.12

Qy	27	VELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFLFRYIL	86
		: : : : :	
Db	6	VKLNVG GTVFETL KSTLTK--HDGFFKALI---ETDVPAEKDDSNCFIDRSPKH FETVL	60
Qy	87	DYLRDRQVVL PDHFPEKGR LKREAEYFQLPDLVKLLTPDEIKQSPDEFCHSD FEDASQGS	146
		: : : : : :	
Db	61	NYMRSGDVVL PDSK KDMLEL KKEAEY YLLSNLAKLCQP-----PTDNF-----	103
Qy	147	DTRICPPSSLL----PADRK-----WG FITVGYRGSCTLGREGQADAK	185
		: : : :	


```

Db      104 --KTCTPEELMRVVANTDKKVIMINYLTYNLNGELVFYPWGFNLVHF---LIQNRDYVEDVY 158
Qy      186 FRRVPRILVCGRISLAKEVFGETLINESRDPDRAP-----ERYTSRFYLKFKHLERAFDM- 239
      |||                               ||: |: |      :| | : | |
Db      159 FRR-----TESQYPEDGPFPEKPYWTFLVYNSTRSGRRPFRHT 197
Qy      240 --LSECGFHM 247
      | :| ||
Db      198 VDLEDCMGHM 207

```

RESULT 3

T15820

hypothetical protein C52B11.2 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C;Accession: T15820

R;Martin, J.

submitted to the EMBL Data Library, November 1995

A;Description: The sequence of *C. elegans* cosmid C52B11.

A;Reference number: Z18411

A;Accession: T15820

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-272 <MAR>

A;Cross-references: EMBL:U41276; NID:g1086884; PID:g1086886; PIDN:AAA82468.1;

CESP:C52B11.2

A;Experimental source: strain Bristol N2

C;Genetics:

A;Gene: CESP:C52B11.2

A;Introns: 12/1; 91/3; 190/3; 221/3

```

Query Match          6.9%; Score 158.5; DB 2; Length 272;
Best Local Similarity 32.3%; Pred. No. 2.5e-05;
Matches 40; Conservative 26; Mismatches 43; Indels 15; Gaps 4;

```

```

Qy      27 VELNVGGQVYFTRHSTLISIPHSLLWKMFSKPRDTANDLAKDSKGRFFIDRDGFLFRYIL 86
      | |||||:|: | |||: | | |:: : | :| | : ||| | ||
Db      84 VRLNVGGKVFQTTTRSTLMREPCSFLYRLCQDEMGLPTD--RDETGAYLIDRDPDFFSPIL 141
Qy      87 DYLRDRQVVLDPDHFPEKGRLKREAEYFQLPDLVKLL-----TPDEIKQSPDEF----- 134
      :||| :::: | :| | ||::: || | :| : :| : :|
Db      142 NYLRHGKLMNPGLSEEGIL-AEADFYNLPSLSQLIMDRIQDRENSVKDATNKFVYRVLQ 200
Qy      135 CHSD 138
      || :
Db      201 CHEE 204

```

RESULT 4

T32221

hypothetical protein T23B12.6 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C;Accession: T32221

R;Davidson, S.; Wohldmann, P.; Gillam, B.

submitted to the EMBL Data Library, September 1997

A;Description: The sequence of *C. elegans* cosmid T23B12.
 A;Reference number: Z21137
 A;Accession: T32221
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-670 <DAV>
 A;Cross-references: EMBL:AF022982; PIDN:AAB69932.1; GSPDB:GN00023; CESP:T23B12.6
 A;Experimental source: strain Bristol N2; clone T23B12
 C;Genetics:
 A;Gene: CESP:T23B12.6
 A;Map position: 5
 A;Introns: 87/2; 185/3; 293/1; 400/1; 457/1; 540/2; 635/3

Query Match 6.9%; Score 158; DB 2; Length 670;
 Best Local Similarity 41.8%; Pred. No. 8.8e-05;
 Matches 41; Conservative 15; Mismatches 36; Indels 6; Gaps 2;

```
Qy      26 VVELNVGGQVYFTRHSTLISIPHSLLWKMFS PKRDTANDLAKDSKGRFFIDRDGFLFRYI 85
          :| |||||::: | :|| || | : | : :: || | |||| | || |
Db      20 IVNLNVGGRIFATSCNTLTWIPDSFFTSLLSGRMNS----VKDPSGAIFIDRDPDLFRVI 75

Qy      86 LDYLRDRQVVLDPDHFPEKGRLKREAEYFQLPDLVKLLT 123
          |:||| :|| | : || || :| | |:: ||
Db      76 LNYLR TKQVDLCG--IKVDTLKHEALFFGLTPLIRRLT 111
```

RESULT 5

T20366

hypothetical protein D2045.8 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T20366

R;Lloyd, C.

submitted to the EMBL Data Library, August 1994

A;Reference number: Z19262

A;Accession: T20366

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-220 <WIL>

A;Cross-references: EMBL:Z35639; PIDN:CAA84696.1; GSPDB:GN00021; CESP:D2045.8

A;Experimental source: clone D2045

C;Genetics:

A;Gene: CESP:D2045.8

A;Map position: 3

A;Introns: 39/3; 127/3; 169/1; 194/3

Query Match 6.8%; Score 156; DB 2; Length 220;
 Best Local Similarity 37.8%; Pred. No. 3e-05;
 Matches 42; Conservative 21; Mismatches 42; Indels 6; Gaps 3;

```
Qy      26 VVELNVGGQVYFTRHSTLISIPHSLLWKMFS PKRDTANDLAKDSKGRFFIDRDGFLFRYI 85
          :|:|:||||::: | || | :| || | : | : :| |||| | || |
Db      6 IVKLDVGGKIFKTTIFTLCK-HDSMLKTMFC----TDVPVTKNEEGSVFIDRDSKHFRLI 60

Qy      86 LDYLRDRQVVLDPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQSPDEFCH 136
          |:||| |: || | : || || | |:: | : ::|| : : |
Db      61 LNFLRDGQIALPDSDEVREVLAEASYFLLDPLIE-LCGERLEQSLNPYYH 110
```

RESULT 6

T33592

hypothetical protein C40A11.7 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 20-Jun-2000

C;Accession: T33592

R;Maggi, L.; Goela, D.

submitted to the EMBL Data Library, October 1998

A;Description: The sequence of *C. elegans* cosmid C40A11.

A;Reference number: Z21374

A;Accession: T33592

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-220 <MAG>

A;Cross-references: EMBL:AF099914; PIDN:AAC68762.1; GSPDB:GN00020; CESP:C40A11.7

A;Experimental source: strain Bristol N2; clone C40A11

C;Genetics:

A;Gene: CESP:C40A11.7

A;Map position: 2

A;Introns: 40/3; 123/3; 162/1

C;Superfamily: *Caenorhabditis elegans* hypothetical protein ZC239.12

Query Match 6.4%; Score 146.5; DB 2; Length 220;

Best Local Similarity 38.4%; Pred. No. 0.00018;

Matches 38; Conservative 13; Mismatches 43; Indels 5; Gaps 1;

Qy 26 VVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDNTANDLAKDSKGRFFIDRDGFLFRYI 85

:|:||||| |: | ||| | :| : ||: :|||| | :

Db 7 IVKLVNVGGSVFETWKSTLTKQD-----GFFKTLVETNIPVKKDTSDCYFIDRSPKYFETV 61

Qy 86 LDYLRDRQVVLDPDHFPEKGRLKREAEYFQLPDLVKLLTP 124

|:|:| |||| | ||:||||: | || | |

Db 62 LNYMRSGVTLPDSEKELQELKKEAEFYLLLEQLVDLCEP 100

RESULT 7

A41784

tumor necrosis factor-alpha-induced protein B12 - human

C;Species: *Homo sapiens* (man)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 29-Aug-1997

C;Accession: A41784

R;Wolf, F.W.; Marks, R.M.; Sarma, V.; Byers, M.G.; Katz, R.W.; Shows, T.B.;
Dixit, V.M.

J. Biol. Chem. 267, 1317-1326, 1992

A;Title: Characterization of a novel tumor necrosis factor-alpha-induced
endothelial primary response gene.

A;Reference number: A41784; MUID:92112779; PMID:1370465

A;Accession: A41784

A;Molecule type: mRNA

A;Residues: 1-348 <WOL>

A;Note: sequence extracted from NCBI backbone (NCBIN:76547, NCBIP:76550)

A;Note: it is uncertain whether Met-1 or Met-33 is the initiator

C;Genetics:

A;Gene: GDB:TNFAIP1

A;Cross-references: GDB:127514; OMIM:191161

A;Map position: 17q22-17q23
A;Start codon: CTG

```
Query Match          6.4%;  Score 146;  DB 2;  Length 348;
Best Local Similarity 22.2%;  Pred. No. 0.00035;
Matches    72;  Conservative    43;  Mismatches 101;  Indels   108;  Gaps    16;

Qy      15  QGSAVPNSFPEVVELNVGGQVYF-----TRHSTLISIPHSLLWKMFSPKRDTANDLAKD  68
          :|  : | :  |:||||| :|:  ||| |::  ||| :  :: |
Db      53  KGGGLGNKY---VQLNVGGSlyyTTVRALTRHDTMLK-----AMFSGRM-----EVLTD  98

Qy      69  SKGRFFIDRDGFLFRYILDYLRDRQVVLDPHFPEKGRLEAEYFQLPDLVKLLTPDEIK 128
          :|  ||| | |  ||:|||| : || : |  |  ||:|: : || :
Db      99  KEGWILIDRCGKHFGTILNYLRDDTITLPQNRQEIKELMAEAKYYLIQGLVNM----- 151

Qy     129  QSPDEFCHSDFEDASQGS DTRICPPSSLLPADRKWGFITVGYRG SCTLGREGQADAKFRR 188
          | | :|  | : | :  | : | :  :
Db     152  -----CQSALQDKKD-----SYQPVCNI-----PIITSLKE 177

Qy     189  VPRILVCGRISLAKEVFGETL NESRDPDRAPERYTSRF--YLKFKHLERAFDMLSECGFH 246
          |::  : | :: : |:  |||  :| |::| || ||
Db     178  EERLIESSTKPVVKLLYNRSNNK-----YSYTSNSDDHL-LKNIE-LFDKLS----- 222

Qy     247  MVACNSSVTASF INQYTDDKI--WSSYTEYVFYREPSRWSPSHCDCCCKNGKGDKEGESG 304
          : | |  ||  |:|  || |  | :| | |
Db     223  -LRFNGRVL--FIKDVIGDEICCSFY-----GQGRKLAE--- 254

Qy     305  TSCNDLSTSSCDSQSEASSPQETV 328
          | : :: |:| |: :
Db     255  VCCTSIVYATEKKQTKVEFPEARI 278
```

RESULT 8

T33590

hypothetical protein C40A11.6 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jul-2000

C;Accession: T33590

R;Maggi, L.; Goela, D.

submitted to the EMBL Data Library, October 1998

A;Description: The sequence of *C. elegans* cosmid C40A11.

A;Reference number: Z21374

A;Accession: T33590

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-179 <MAG>

A;Cross-references: EMBL:AF099914; PIDN:AAC68757.1; GSPDB:GN00020; CESP:C40A11.6

A;Experimental source: strain Bristol N2; clone C40A11

C;Genetics:

A;Gene: CESP:C40A11.6

A;Map position: 2

A;Introns: 40/3; 123/3

C;Superfamily: *Caenorhabditis elegans* hypothetical protein ZC239.12

```
Query Match          6.4%;  Score 145.5;  DB 2;  Length 179;
Best Local Similarity 38.4%;  Pred. No. 0.00016;
Matches    38;  Conservative    13;  Mismatches  43;  Indels     5;  Gaps     1;
```

```

Qy      26 VVELNVGGQVYFTRHSTLISIPHSLLWKMFS PKRDTANDLAKDSKGRFFIDRDGFLFRYI 85
      :|:||||| |: | ||| | :| : ||: :|||| | :
Db      7 IVKLVGGSVFETWKTSTLTQD-----GFFKTLIETNVPVKKDTSDCYFIDRSPKYFETV 61

Qy      86 LDYLRDRQVVLDPDHFPEKGR LKREAEYFQLPDLVKLLTP 124
      |:|:| ||| | ||:||||: | || | |
Db      62 LNYMRSGVTVLPDSEKELQELKKEAEFYLLLEHLVDLCEP 100

```

RESULT 9

T31997

hypothetical protein B0281.6 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jul-2000

C;Accession: T31997

R;Pauley, A.; Scheet, P.

submitted to the EMBL Data Library, July 1997

A;Description: The sequence of *C. elegans* cosmid B0281.

A;Reference number: Z21109

A;Accession: T31997

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-212 <PAU>

A;Cross-references: EMBL:AF016666; PIDN:AAB66085.1; GSPDB:GN00020; CESP:B0281.6

A;Experimental source: strain Bristol N2; clone B0281

C;Genetics:

A;Gene: CESP:B0281.6

A;Map position: 2

A;Introns: 40/3; 121/3; 160/1

C;Superfamily: *Caenorhabditis elegans* hypothetical protein ZC239.12

```

Query Match          6.3%; Score 144; DB 2; Length 212;
Best Local Similarity 38.5%; Pred. No. 0.00027;
Matches 45; Conservative 10; Mismatches 44; Indels 18; Gaps 4;

```

```

Qy      22 SFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFS PKRDTANDLAKDSKGRFFIDRDGFL 81
      | :|:||||| |: | ||| | ::| | | || |||||
Db      3 SSESIVKLVGGTVFVTLKSTLTQ--HHGIFKALVKTEMPAED--GDS---FFIDRSPKH 55

Qy      82 FRYILDYLRDRQVVLDPDHFPEKGR LKREAEYFQLPDLVKLL-----TPDEI 127
      | :|:|:| | ||| | |||||: | | | | ||:
Db      56 FETVLNYYIRSGDVDLPDSENELKELKREAEYYSLEKLATLCQSSMPKIKSYKTADEL 112

```

RESULT 10

T26685

hypothetical protein F18A11.5 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T26685

R;Wallis, J.

submitted to the EMBL Data Library, October 1998

A;Reference number: Z20253

A;Accession: T26685

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-373 <WIL>
A;Cross-references: EMBL:AL032639; PIDN:CAA21638.1; GSPDB:GN00020; CESP:F18A11.5
A;Experimental source: clone Y38F1A
C;Genetics:
A;Gene: CESP:F18A11.5
A;Map position: 2
A;Introns: 7/3; 44/3; 99/3; 152/2; 198/3; 223/1

Query Match 5.8%; Score 131.5; DB 2; Length 373;
Best Local Similarity 32.5%; Pred. No. 0.0059;
Matches 40; Conservative 20; Mismatches 40; Indels 23; Gaps 4;

```
Qy      8 SRYYPREQGSAVPNSFPEVVVELNVGGQVYFTRHSTLISIPHSLLWKMFSFKRDTANDLAK 67
      | : :| || : | | |||||: : | :|| : :| | | : | ::
Db      7 SMTFSQEGGS-----NLSEVLLNVGGKKFETT VATL TRVSDTVLAVMVSDRWKTGDEI-- 60

Qy     68 DSKGRFFIDRDGFLFRYILDYLRDRQVVLDPHFPEKG-----RLKREAEYFQLPDLVKL 121
      ||||| | :|:|||| ||| ||||| : : | | : :
Db     61 -----FIDRDPKHFGKVLNYLRD-----GDHFVAPSDTEACDELKREAHFYNMPFLAEM 109

Qy     122 LTP 124
      |
Db     110 CMP 112
```

RESULT 11

T32070

hypothetical protein F22E5.6 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 20-Jun-2000

C;Accession: T32070

R;Graves, T.; Wohldmann, P.; Clarke, K.

submitted to the EMBL Data Library, July 1997

A;Description: The sequence of *C. elegans* cosmid F22E5.

A;Reference number: Z21119

A;Accession: T32070

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-231 <GRA>

A;Cross-references: EMBL:AF016681; PIDN:AAB66172.1; GSPDB:GN00020; CESP:F22E5.6

A;Experimental source: strain Bristol N2; clone F22E5

C;Genetics:

A;Gene: CESP:F22E5.6

A;Map position: 2

A;Introns: 40/3; 125/3; 170/1

C;Superfamily: *Caenorhabditis elegans* hypothetical protein ZC239.12

Query Match 5.4%; Score 122.5; DB 2; Length 231;
Best Local Similarity 24.2%; Pred. No. 0.017;
Matches 46; Conservative 21; Mismatches 66; Indels 57; Gaps 4;

```
Qy     25 EVVELNVGGQVYFTRHSTLISIPHSLLWKMFSFKRDTANDLAKDSKGRFFIDRDGFLFRY 84
      | : ||:| | :: | ||| | :| : || |||| |
Db      6 EKIRLNIGGTIFETSKSTLT KFD-----GFFKTLLETDIPIQKDDSNCFIDRS PRHFEK 60

Qy     85 ILDYLRDRQV--LPDHFPEKGRLKREAEYFQLPDLVK----- 120
      ||:|||| | ||: | : :||::: | |::
```

```

Db          61 ILNYLRDGADVDLLPESEKEVREILKEAQFYLLLEGLMELCKRSSCKIRTFESYHLLKLI 120
Qy          121 -----LLTPDEIKQSPDEFCHSDFEDASQGS-----DTRICP 152
              |: : | |: | || : || :|
Db          121 AEAGKPVLMFYLVKDNRIHVHPNNFEFLDFLEKHQGKLDIYFSEFGQKKESPYETHQN 180
Qy          153 PSSLLPADRK 162
              || || |:
Db          181 PSQFLPPGRE 190

```

RESULT 12

T33589

hypothetical protein C40A11.3 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C;Accession: T33589

R;Maggi, L.; Goela, D.

submitted to the EMBL Data Library, October 1998

A;Description: The sequence of *C. elegans* cosmid C40A11.

A;Reference number: Z21374

A;Accession: T33589

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-236 <MAG>

A;Cross-references: EMBL:AF099914; PIDN:AAC68765.1; GSPDB:GN00020; CESP:C40A11.3

A;Experimental source: strain Bristol N2; clone C40A11

C;Genetics:

A;Gene: CESP:C40A11.3

A;Map position: 2

A;Introns: 40/3; 124/3; 163/1; 196/3

```

Query Match          5.4%; Score 122.5; DB 2; Length 236;
Best Local Similarity 35.4%; Pred. No. 0.018;
Matches 34; Conservative 15; Mismatches 42; Indels 5; Gaps 1;

```

```

Qy          26 VVELNVGGQVYFTRHSTLISIPHSLLWKMFSFKRDTANDLAKDSKGRFFIDRDGFLFRYI 85
              :: ||: || |: | :|| | | :| || ||| | |
Db          7 IMMLNIGGTVFHTSKATLTGIN-----GFFKMLLES DIPLHKDESNCIFIDRSPKHFDVI 61
Qy          86 LDYLRDRQVVLDPHFPEKGRLKREAEYFQLPDLVKL 121
              |::||| | ||: | ::|||::: | || |
Db          62 LNFLRDGDVDLPELEKEVKEVRREAQFYLLDGLVYL 97

```

RESULT 13

T25978

hypothetical protein ZC239.15 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000

C;Accession: T25978

R;Wu, X.; Kramer, J.

submitted to the EMBL Data Library, December 1996

A;Description: The sequence of *C. elegans* cosmid ZC239.

A;Reference number: Z20117

A;Accession: T25978

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA
A;Residues: 1-246 <WUX>
A;Cross-references: EMBL:U80842; PIDN:AAB37955.1; GSPDB:GN00020; CESP:ZC239.15
A;Experimental source: strain Bristol N2; clone ZC239
C;Genetics:
A;Gene: CESP:ZC239.15
A;Map position: 2
A;Introns: 37/3; 127/3
C;Superfamily: Caenorhabditis elegans hypothetical protein ZC239.12

Query Match 5.3%; Score 121.5; DB 2; Length 246;
Best Local Similarity 32.2%; Pred. No. 0.023;
Matches 38; Conservative 19; Mismatches 52; Indels 9; Gaps 3;

```
Qy      25 EVVELNVGGQVYFTRHSTLISIPHSLLWKMFSKPRDTANDLAKDSKGRFFIDRDGFLFRY 84
      | |::||| :: | |||          | :: | | | ||| |
Db      3 ETVKLDVGGTIFKTSRSTLTKEF-----GFFKTMLESDIGLKIDESGSIFIDRSPKNFDL 57

Qy      85 ILDYLRDRQVVLDPDHFPEKGRLKREAEYFQLPDLVKLLTPD-EIKQSPD---EFCHSD 138
      ||::|| | |||: : | ||::| | |::| |::| | ||
Db      58 ILNFMRDGDVVLNCELKLLKELLVEAQFYLLDGLIELCNSKIELVEAPKIKLRFIESD 115
```

RESULT 14

T21630

hypothetical protein F32B4.5 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000

C;Accession: T21630

R;White, S.

submitted to the EMBL Data Library, November 1996

A;Reference number: Z19452

A;Accession: T21630

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-277 <WIL>

A;Cross-references: EMBL:Z81522; PIDN:CAB04230.1; GSPDB:GN00019; CESP:F32B4.5

A;Experimental source: clone F32B4

C;Genetics:

A;Gene: CESP:F32B4.5

A;Map position: 1

A;Introns: 131/3; 237/3

C;Superfamily: Caenorhabditis elegans hypothetical protein F32B4.5

Query Match 5.2%; Score 119; DB 2; Length 277;
Best Local Similarity 24.1%; Pred. No. 0.042;
Matches 58; Conservative 28; Mismatches 75; Indels 80; Gaps 10;

```
Qy      33 GQVYFTRHSTLISIPHSLLWKMFSKPRDTANDLAKDSKGRFFIDRDGFLFRYILDYLR-- 90
      | | :|| | |||          |: | ||          | : | ::| ||
Db      69 GATISTTRATLQRAPQSLL-----ATSPDATSDS-----DDKIVRIILVEALRRS 112

Qy      91 DRQVVLDPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQSPDEFCHSDFEDASQGS DTRI 150
      | :: : | : || ||: | |: | | | ||:          | ||
Db      113 DMSIIVSESFQWARLAVEAKRLGLISFVEAAC PSTISIS----CHAAL-----STGRI 162

Qy      151 CPPSSLLPADRKWGFITVGYRG SCTLGR-----EGQADAKF----- 186
```



```

      | :      ||      : :      | | :      : |      : |
Db      163 NPEVTF-----RK--VHNIHFMAQKTTGKAFASSNPEPVKGTTSPPFFLLSFFFFPFFCSFL 216
Qy      187 -----RRVPRIILVCGRISLAKEVFGETLINESRD---PDRAPERYTS 224
      | ||:| |:: : : |||::||| ||      | :|||
Db      217 LRFSPINFPLLLLMNTAIGEYVLRIVVSGKVIMCRAVFGDSLNECRDGGGTDGFEMDRYTS 276
Qy      225 R 225
      |
Db      277 R 277

```

RESULT 15

T32065

hypothetical protein F22E5.8 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C;Accession: T32065

R;Graves, T.; Wohldmann, P.; Clarke, K.

submitted to the EMBL Data Library, July 1997

A;Description: The sequence of *C. elegans* cosmid F22E5.

A;Reference number: Z21119

A;Accession: T32065

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-134 <GRA>

A;Cross-references: EMBL:AF016681; PIDN:AAB66174.1; GSPDB:GN00020; CESP:F22E5.8

A;Experimental source: strain Bristol N2; clone F22E5

C;Genetics:

A;Gene: CESP:F22E5.8

A;Map position: 2

A;Introns: 37/3

```

Query Match          5.1%; Score 115.5; DB 2; Length 134;
Best Local Similarity 35.1%; Pred. No. 0.031;
Matches 34; Conservative 16; Mismatches 42; Indels 5; Gaps 2;

```

```

Qy      25 EVVELNVGGQVYFTRHSTLISIPHSLLWKMFSFKRDTANDLAKDSKGRFFIDRDGFLFRY 84
      | |::||| :: | |||      : | |      :: | | | ||| |
Db      3 ETVQLDVGGTIFKTSKSTLTKE-NGFLKIML----ESDIGLKIDESGSIFIDRSPKHFDL 57
Qy      85 ILDYLRDRQVVLDPHFPEKGRLLKREAEIFQLPDLVKL 121
      ||::|| | |||      | ||:: | :||:|
Db      58 ILNFMRDGDVVLPSCELTVKELLAEAQFYLLDELIEL 94

```

Search completed: January 29, 2004, 02:55:49

Job time : 31 secs

OM protein - protein search, using sw model

Run on: January 28, 2004, 23:02:20 ; Search time 18 Seconds
 (without alignments)
 1118.191 Million cell updates/sec

Title: US-10-056-884A-2
 Perfect score: 2284
 Sequence: 1 MALSGNCSRYYPREQGSAVP.....DRFPERKHPWQSELLRKHYHL 428

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		DB	ID	Description
	Score	Match Length			
1	146.5	6.4 265	1	Y176_HUMAN	Q14681 homo sapien
2	146	6.4 316	1	TNP1_HUMAN	Q13829 homo sapien
3	105	4.6 1504	1	DPOZ_YEAST	P14284 saccharomyc
4	104.5	4.6 1176	1	NIR_NEUCR	P38681 neurospora
5	104	4.6 490	1	CIKL_DROME	P17971 drosophila
6	103.5	4.5 140	1	YR43_CAEEL	Q09389 caenorhabdi
7	102	4.5 491	1	KCS3_RAT	O88759 rattus norv
8	101.5	4.4 1537	1	DNM1_CHICK	Q92072 gallus gall
9	100	4.4 491	1	KCS3_HUMAN	Q9bq31 homo sapien
10	100	4.4 737	1	ADDA_HUMAN	P35611 homo sapien
11	99	4.3 491	1	KCS3_RABIT	Q9tt17 oryctolagus
12	98	4.3 329	1	IRF1_MOUSE	P15314 mus musculu
13	98	4.3 825	1	SWI3_YEAST	P32591 saccharomyc
14	97.5	4.3 1213	1	FMN_CHICK	Q05858 gallus gall
15	96.5	4.2 1186	1	PKCB_HUMAN	Q9ulu4 homo sapien
16	96.5	4.2 3695	1	LMA5_HUMAN	O15230 homo sapien
17	95	4.2 1023	1	STR8_HUMAN	Q92502 homo sapien

18	95	4.2	3390	1	POLG_DEN3	P27915	d genome po
19	94	4.1	548	1	CNE2_MOUSE	P59108	mus musculu
20	93	4.1	601	1	YE06_SCHPO	O13803	schizosacch
21	92	4.0	352	1	P53_ORYLA	P79820	oryzias lat
22	92	4.0	768	1	RGL1_MOUSE	Q60695	mus musculu
23	91.5	4.0	3767	1	MUA3_CAEEL	P34576	caenorhabdi
24	91	4.0	1275	1	GMRP_HUMAN	Q13972	homo sapien
25	91	4.0	1969	1	Z292_HUMAN	O60281	homo sapien
26	91	4.0	3083	1	POLG_ZYMVS	O36979	z genome po
27	90	3.9	357	1	CHLI_SYNY3	P51634	synechocyst
28	90	3.9	793	1	ATK1_ARATH	Q07970	arabidopsis
29	89.5	3.9	640	1	ELM1_YEAST	P32801	saccharomyc
30	89.5	3.9	1015	1	DNL3_MOUSE	P97386	mus musculu
31	89.5	3.9	5038	1	PCLO_MOUSE	Q9qyx7	mus musculu
32	89	3.9	523	1	CIK3_HUMAN	P22001	homo sapien
33	89	3.9	683	1	YKB7_YEAST	P34243	saccharomyc
34	89	3.9	705	1	YNP9_CAEEL	P34562	caenorhabdi
35	89	3.9	2476	1	ATRX_MOUSE	Q61687	mus musculu
36	88.5	3.9	283	1	YQVW_CAEEL	Q17439	caenorhabdi
37	88.5	3.9	538	1	Z306_HUMAN	Q9brr0	homo sapien
38	88.5	3.9	625	1	CIKG_RAT	Q63734	rattus norv
39	88	3.9	3829	1	SACS_HUMAN	Q9nzt4	homo sapien
40	87.5	3.8	477	1	GATB_MYCPN	P75533	mycoplasma
41	87.5	3.8	486	1	WHI2_YEAST	P12611	saccharomyc
42	87.5	3.8	664	1	PLB1_YEAST	P39105	saccharomyc
43	87	3.8	249	1	YAT6_RHOBL	P05449	rhodopseudo
44	87	3.8	345	1	YAYE_SCHPO	Q10221	schizosacch
45	87	3.8	1565	1	DMN_HUMAN	O15061	homo sapien

ALIGNMENTS

RESULT 1

Y176_HUMAN

ID Y176_HUMAN STANDARD; PRT; 265 AA.

AC Q14681;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical protein KIAA0176 (Fragment).

GN KIAA0176.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Bone marrow;

RX MEDLINE=96281124; PubMed=8724849;

RA Nagase T., Seki N., Ishikawa K.-I., Tanaka A., Nomura N.;

RT "Prediction of the coding sequences of unidentified human genes. V.

RT The coding sequences of 40 new genes (KIAA0161-KIAA0200) deduced by

RT analysis of cDNA clones from human cell line KG-1.";

RL DNA Res. 3:17-24(1996).

CC -!- SIMILARITY: Contains 1 BTB/POZ domain.

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CC -----

DR EMBL; D79998; BAA11493.1; -.
DR InterPro; IPR000210; BTB_POZ.
DR InterPro; IPR003131; K_tetra.
DR Pfam; PF02214; K_tetra; 1.
DR SMART; SM00225; BTB; 1.
DR PROSITE; PS50097; BTB; FALSE_NEG.
KW Hypothetical protein.
FT NON_TER 1 1
FT DOMAIN 74 174 BTB.
SQ SEQUENCE 265 AA; 28801 MW; 5C7455CCBBEE8924 CRC64;

Query Match 6.4%; Score 146.5; DB 1; Length 265;
Best Local Similarity 30.2%; Pred. No. 0.00026;
Matches 51; Conservative 25; Mismatches 68; Indels 25; Gaps 8;

QY 27 VELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFLFRYIL 86
| | | | | : | | | | | : : | | | | : | | | | |
Db 76 VRLNVGGTYFVTTTQTLGREPKSFLCRLCC-QEDPELDSKDDETGayLIDRDPTYFGPIL 134

QY 87 DYLRDRQVVLDPDHFPEKGRLLKREAEYFQLPDLVKLLTPDEIKQSPDEFCHSDFEDASQGS 146
: | | | : : : : | : | : | | : : : | | : : : : | | |
Db 135 NYLRHGKLIITKELAEEGVLE-EAEFYNIASIVRLV-KERIRDNENR-----TSQGP 184

QY 147 DTRI-----CPPSSLL----PADRKWGF---ITVGYRGSGTLGREGQAD 183
: | | | | | | | | : : | | | | : : | | | | :
Db 185 VKHVYRVLQCQEEELTQMVSTMSDGWKFEQLISIG--SSYNYGNEDQAE 231

RESULT 2

TNP1_HUMAN

ID TNP1_HUMAN STANDARD; PRT; 316 AA.
AC Q13829;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor, alpha-induced protein 1, endothelial (B12
DE protein).
GN TNFAIP1 OR EDP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Endothelial cells;
RX MEDLINE=92112779; PubMed=1370465;
RA Wolf F.W., Marks R.M., Sarma V., Byers M.G., Katz R.W., Shows T.B.,
RA Dixit V.M.;
RT "Characterization of a novel tumor necrosis factor-alpha-induced

RT endothelial primary response gene.";
 RL J. Biol. Chem. 267:1317-1326(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
 RA Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- INDUCTION: BY TNF-ALPHA, INTERLEUKIN-1 BETA AND LIPOPOLYSACCHARIDE
 CC (LPS).
 CC -!- SIMILARITY: Contains 1 BTB/POZ domain.
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 CC -----
 DR EMBL; M80783; AAA58385.1; -.
 DR EMBL; AY065346; AAL38649.1; -.
 DR EMBL; BC001643; AAH01643.1; -.
 DR EMBL; BC001949; AAH01949.1; -.
 DR Genew; HGNC:11894; TNFAIP1.
 DR MIM; 191161; -.
 DR InterPro; IPR000210; BTB_POZ.
 DR InterPro; IPR003131; K_tetra.
 DR Pfam; PF02214; K_tetra; 1.
 DR SMART; SM00225; BTB; 1.
 DR PROSITE; PS50097; BTB; 1.
 FT DOMAIN 28 96 BTB.
 SQ SEQUENCE 316 AA; 36204 MW; D20B810A00507DCF CRC64;

Query Match 6.4%; Score 146; DB 1; Length 316;
 Best Local Similarity 22.2%; Pred. No. 0.00036;
 Matches 72; Conservative 43; Mismatches 101; Indels 108; Gaps 16;

```

Qy      15 QGSAVPNSFPEVVELNVGGQVYF-----TRHSTLISIPHSLLWKMFSPKRDTANDLAKD 68
      :| : | : | :| | | | :| : | | | : | :| : | :| :|
Db      21 KGGGLGNKY---VQLNVGGSlyyTtVRALTRHDTMLK-----AMFSGRM---EVLTD 66

Qy      69 SKGRFFIDRDGFLFRYILDYLRDRQVVLDPHFPEKGRLKREAEYFQLPDLVKLLTPDEIK 128
      :| | | | | | | | | :| :| :| :| :| :| :| :| :|
Db      67 KEGWILIDRCGKHFGTILNLYLRDDTITLPQNRQEIKELMAEAKYyliQGLVNM----- 119

Qy     129 QSPDEFCHSDFEDASQGSdTRICPPSSLLPADRKWGFITVGYRGsCTLGREGQADAKFRR 188
      | | :| | | | | | | | | | | | | | | | | | | | |
Db     120 -----CQSALQDKKD-----SYQPVCNI----PIITSLKE 145

Qy     189 VPRILVCGRISLAKEVFGETLINESRDPDRAPERYTSRF--YLKFKHLERAFDMLSECGFH 246
      | : : | : : : | : | | | :| | :| | | |
Db     146 EERLIESSTKPVVKLLYNRSNNK-----YSYTSNSDDHL-LKNIE-LFDKLS----- 190

Qy     247 MVACNSSVTASFINQYTDdKI--WSSyTEYVFYREPSRWSPSHCDCCCKNGKGDKEGESG 304
      : | | | | | | | | | | | | | | | | | | | |
Db     191 -LRFNGRVL--FIKdVIGDEICCSWsfY-----GQGRKLAE-- 222

Qy     305 TSCNDLSTSSCDsQSEASSPQETV 328
      | : : : | : : | : :
Db     223 VCCTsIVYATEKKQTKVEFPEARi 246
  
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RESULT 3

DPOZ_YEAST

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ID  DPOZ_YEAST      STANDARD;      PRT; 1504 AA.
AC  P14284;
DT  01-JAN-1990 (Rel. 13, Created)
DT  01-JAN-1990 (Rel. 13, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  DNA polymerase zeta catalytic subunit (EC 2.7.7.7).
GN  REV3 OR PSO1 OR YPL167C OR P2535.
OS  Saccharomyces cerevisiae (Baker's yeast).
OC  Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC  Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX  NCBI_TaxID=4932;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=90008808; PubMed=2676986;
RA  Morrison A., Christensen R.B., Alley J., Beck A.K., Bernstine E.G.,
RA  Lemontt J.F., Lawrence C.W.;
RT  "REV3, a Saccharomyces cerevisiae gene whose function is required for
RT  induced mutagenesis, is predicted to encode a nonessential DNA
RT  polymerase.";
RL  J. Bacteriol. 171:5659-5667(1989).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=S288c / AB972;
RX  MEDLINE=97103777; PubMed=8948103;
RA  Purnelle B., Coster F., Goffeau A.;
RT  "The sequence of 55 kb on the left arm of yeast chromosome XVI
  
```

RT identifies a small nuclear RNA, a new putative protein kinase and two
RT new putative regulators.";
RL Yeast 12:1483-1492(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
RX MEDLINE=97313271; PubMed=9169875;
RA Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansorge W.,
RA Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,
RA Botstein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M.,
RA Chung E., Churcher C.M., Coster F., Davis K., Davis R.W.,
RA Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A.,
RA Duncan M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A.,
RA Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.,
RA Hunicke-Smith S., Hyman R., Johnston M., Kalman S., Kleine K.,
RA Komp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J.,
RA Marathe R., Messenguy F., Mewes H.-W., Mirtipati S., Moestl D.,
RA Mueller-Auer S., Namath A., Nentwich U., Oefner P., Pearson D.,
RA Petel F.X., Pohl T.M., Purnelle D., Schafer M., Scharfe M.,
RA Scherens B., Schramm S., Schroeder M., Sdicu A.M., Tettelin H.,
RA Urrestarazu L.A., Ushinsky S., Vierendeels F., Vischers S., Voss H.,
RA Walsh S.V., Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E.,
RA Zhong W.W., Zollner A., Vo D.H., Hani J.;
RT "The nucleotide sequence of *Saccharomyces cerevisiae* chromosome XVI.";
RL Nature 387:103-105(1997).
CC -!- FUNCTION: REQUIRED FOR INDUCED MUTAGENESIS, IT IS A NONESSENTIAL
CC DNA POLYMERASE. IT MAY FUNCTION IN TRANSLESION SYNTHESIS.
CC TRANSLESION SYNTHESIS IN *S.CEREVISIAE* MAY USE A SPECIALIZED DNA
CC POLYMERASE THAT IS NOT REQUIRED FOR OTHER DNA REPLICATIVE
CC PROCESSES.
CC -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + {DNA}(N).
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-B FAMILY.
CC -----
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CC -----
DR EMBL; M29683; AAA34968.1; -.
DR EMBL; X96770; CAA65554.1; -.
DR EMBL; Z73523; CAA97873.1; -.
DR PIR; A33602; A33602.
DR SGD; S0006088; REV3.
DR InterPro; IPR006172; DNA_pol_B.
DR InterPro; IPR006134; DNA_pol_B_dom.
DR InterPro; IPR006133; DNA_pol_B_exo.
DR Pfam; PF00136; DNA_pol_B; 1.
DR Pfam; PF03104; DNA_pol_B_exo; 1.
DR PRINTS; PR00106; DNAPOLB.
DR SMART; SM00486; POLBc; 1.
DR PROSITE; PS00116; DNA_POLYMERASE_B; 1.
KW Transferase; DNA-directed DNA polymerase; DNA replication;

KW DNA-binding; DNA repair; Nuclear protein; Zinc-finger.
 FT ZN_FING 1398 1417 C4-TYPE (POTENTIAL).
 FT ZN_FING 1446 1473 C4-TYPE (POTENTIAL).
 SQ SEQUENCE 1504 AA; 172956 MW; 54C2C6B664F734F5 CRC64;

Query Match 4.6%; Score 105; DB 1; Length 1504;
 Best Local Similarity 20.2%; Pred. No. 4.5;
 Matches 111; Conservative 67; Mismatches 186; Indels 186; Gaps 26;

```

Qy      12 PREQGSAPVN-----SFP-----EVVELNVGGQVYFT---RHSTLISIPHSL 50
      | | | ||| : | : : ||: | | : :|
Db      49 PLNQFSQVPNIRVFGALPTGHQVLCHVHGILPYMFIKYDGTDTSTLRHQRCQVHKT 108

Qy      51 LWKM---FSPKRDITANDLAKDSKGR-----FFIDRDGFLFRY----- 84
      |: | |:| :|| | | |: | |
Db     109 EVKIRASFKRKKDDKHDLAGDKLGNLNFVADVSVVKGIPFYGYHVGWNLFYKISLLNPSC 168

Qy      85 ---ILDYLRDRQV-----VLPDHFPEKGRLKREAE-----YFQLP----- 116
      | : :|| :: : | | |: | : ||: |
Db     169 LSRISSELIRDGKIFGKKFEIYESHIPY--LLQWTADFNLFGCSWINVDRCYFRSPVLNSI 226

Qy     117 -DLVKLLTPDEIKQSPDEFC-----HSDFEDASQG--SDTRICPP-----SSLLPADR 161
      |: || |::: | || || | : | | | |
Db     227 LDIDKLTINDDLQLLLDRCDFKCNVLSRRDFPRVGNGLIEIDILPQFIKNREKLQHRDI 286

Qy     162 KWGFITVGYRGSTLGGREGQADAKFRRVPRILVCGRISLAKEVFGE-----TLNESR 213
      |: | : | | : | |::: | : | | :
Db     287 HHDFL-----EKLGDISDIPVKPYVSSARDMINELTMQREELSKEYK 329

Qy     214 DPDRAPERYTS-----RFYLFKHLERAFDMLSECGFHMVACNSSVTA----- 256
      :| :|: | || | :| || : : | :|
Db     330 EPPET-KRHVSGHQWQSSGEFEAFYKKAQHKTSTFDGQIPNFENFIDKNQKFSAINTPYE 388

Qy     257 -----SFINQYTDDKIWSSYTEYVFYREPSRWSPSHCDCCCKNGKGDK 299
      | :: ||:: :|:| | | | :
Db     389 ALPQLWPRLPQIEINNNSMQDKKNDDQVNASFTEYEI-----CGVDN---EN 432

Qy     300 EGESGTSCNDLSTSSCDSQSEASSPQETVICGPVTRQTNIQTLDRPIKKGVPVQLIQQSEM 359
      || |:: | | :| || |:: | : | |:: : : |
Db     433 EGVKGSNIKSRSYSWL-PESIASPKDSTILLDHQTKYHN--TINFMS---DCAMTQNMAS 486

Qy     360 RRKSDLLRILTSGSRESNMSSKKKAVK-----EKLSIEEELEKCIQDFLKKKIPDRFP 412
      :|| || | :: | :| | :| | :: : | || | | : ||
Db     487 KRK---LRSSVSANKTSLSRKRKKVMAAGLRYGKRAFYGEPPFGYQDIILNKLEDEGFP 543

Qy     413 --ERKHPWQS 420
      : | | : |
Db     544 KIDYKDPFFS 553

```

RESULT 4

NIR_NEUCR

ID NIR_NEUCR STANDARD; PRT; 1176 AA.

AC P38681;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Nitrite reductase [NAD(P)H] (EC 1.7.1.4).
 GN NIT-6.
 OS *Neurospora crassa*.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; *Neurospora*.
 OX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=74-OR23-1A / FGSC 987;
 RX MEDLINE=93224461; PubMed=8096840;
 RA Exley G.E., Colandene J.D., Garrett R.H.;
 RT "Molecular cloning, characterization, and nucleotide sequence of
 RT nit-6, the structural gene for nitrite reductase in *Neurospora*
 RT *crassa*."
 RL J. Bacteriol. 175:2379-2392(1993).
 CC -!- CATALYTIC ACTIVITY: Ammonium hydroxide + 3 NAD(P)(+) + H(2)O =
 CC nitrite + 3 NAD(P)H.
 CC -!- COFACTOR: THIS ENZYME IS A FAD FLAVOPROTEIN THAT ALSO CONTAINS
 CC A SIROHEME AND ONE 4FE-4S IRON-SULFUR CENTER.
 CC -!- PATHWAY: Nitrate assimilation (denitrification); second step.
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- INDUCTION: By nitrate.
 CC -!- SIMILARITY: THE C-TERMINAL DOMAIN IS A 4FE-4S/SIROHEME DOMAIN
 CC FOUND IN NITRITE REDUCTASES (EC 1.7.1.4 AND EC 1.7.7.1) AND
 CC SULFITE REDUCTASES (EC 1.8.1.2 AND EC 1.8.7.1).
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 CC -----
 DR EMBL; L07391; -; NOT_ANNOTATED_CDS.
 DR PIR; A49848; A49848.
 DR InterPro; IPR001327; FAD_pyr_redox.
 DR InterPro; IPR006066; Nir_Si.
 DR InterPro; IPR006067; Nir_Sir_4Fe4S.
 DR InterPro; IPR005117; Nir_sir_fer.
 DR InterPro; IPR005806; Rieske_dom.
 DR Pfam; PF04324; fer2_BFD; 1.
 DR Pfam; PF01077; NIR_SIR; 1.
 DR Pfam; PF03460; NIR_SIR_ferr; 1.
 DR Pfam; PF00070; pyr_redox; 1.
 DR Pfam; PF00355; Rieske; 1.
 DR PRINTS; PR00368; FADPNR.
 DR PRINTS; PR00397; SIROHAEM.
 DR PROSITE; PS00365; NIR_SIR; 1.
 KW Oxidoreductase; FAD; Flavoprotein; Metal-binding; Iron-sulfur; Iron;
 KW 4Fe-4S; Nitrate assimilation; Heme; NADP.
 FT NP_BIND 26 60 FAD (POTENTIAL).
 FT NP_BIND 183 215 NAD(P)H (POTENTIAL).
 FT METAL 717 717 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
 FT METAL 723 723 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
 FT METAL 757 757 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
 FT METAL 761 761 IRON-SULFUR (4FE-4S) (BY SIMILARITY).

FT METAL 761 761 IRON (SIROHEME AXIAL LIGAND) (BY
 FT SIMILARITY).
 FT DOMAIN 998 1054 PRO/SER-RICH.
 SQ SEQUENCE 1176 AA; 127367 MW; FFC7DCE66F80C710 CRC64;

Query Match 4.6%; Score 104.5; DB 1; Length 1176;
 Best Local Similarity 19.8%; Pred. No. 3.5;
 Matches 85; Conservative 44; Mismatches 122; Indels 179; Gaps 21;

```

Qy      69 SKGRFFIDRDGFLFRYILDYLRDRQVVLDPHFPEKGRLEKRE----- 109
      | | || ||| | | | | | | | | | | | | | | | | | | | | | | |
Db      385 SFGDFFADRDG-----PKELPPK--LRRELKKSGGKAEVKALTYKDPF 425

Qy      110 -----AEYFQLPDLVKL-----LTPDEI----KQSPDEFC 135
      : | : | | | : | : : | : | :
Db      426 LSVYKKYIFTSDGKYLLGGMMIGDITDYVRLVPLVKTHKELDVPPSQLILGAKKSGDDNG 485

Qy      136 HSDFDASQGS DTRICPPSSLLPAD----RKWGFIT-VGYRG SCTLGREGQADAKFRRVP 190
      | | | | : | | : : | | | | : | | | | | | |
Db      486 DDDLDP-----DTQICSCHNVTKADLVAPLKS GECTSLGDLK SCKTAGTG----- 530

Qy      191 RILVCGR-ISLAKEVFGETL----NESRDP--DRAPER YTSRFY--LKFKHLERAFDMLS 241
      || : | : | | : | : : | | : | : | | | : :
Db      531 ----CGGCMPLVTSIFNRTMASLGTEVKNNLCPHFPEYSRADLYNIISVKRLRTLDPV MR 586

Qy      242 ECG-----FHMVACNSSVTASFINQYTDDKIWSSYTEYVFYREPSRWSPSHCDCCCKNGK 296
      | | | | : | : : | : : : | : | : | : |
Db      587 EAGADADSLGCEACKPAIASIFAS-----LWNDHV-----MSPAH-----HGL 624

Qy      297 GDKEGESGTSCNDLSTSSCDSQSEAS--SPQETVICGPVTRQTNIQTLDRPIKKG PVQLI 354
      | : | | : | : | : : : | | : : | : |
Db      625 QDTNDRFMGNIQRNGTFSVVPRAAGEITPEKLIVIGEVAKEYNLYTK----- 672

Qy      355 QQSEMRRKSDLLRILTSGSRESNMSSKKKAVKEKLSIEEELEKCIQDFLK--KKIPDRFP 412
      : | | | : | | | | | | | | | | | |
Db      673 -----ITGGQRIDMFGAKK-----QDLLKIWKKLVDAGM 701

Qy      413 ERKHPWQSEL 422
      | | : |
Db      702 ESGHAYAKSL 711
  
```

RESULT 5

CIKL_DROME

ID CIKL_DROME STANDARD; PRT; 490 AA.
 AC P17971; Q9VW11;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Potassium voltage-gated channel protein Shal (Shal2).
 GN SHAL OR SHAL2 OR CG9262.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=90239553; PubMed=2333511;
 RA Wei A., Covarrubias M., Butler A., Baker K., Pak M., Salkoff L.;
 RT "K⁺ current diversity is produced by an extended gene family
 RT conserved in Drosophila and mouse."
 RL Science 248:599-603(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90245668; PubMed=2336395;
 RA Wei A., Covarrubias M., Butler A., Baker K., Pak M., Salkoff L.;
 RT "Shal, Shab, and Shaw: three genes encoding potassium channels in
 RT Drosophila."
 RL Nucleic Acids Res. 18:2173-2174(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 CC -!- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED

CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K⁺ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT. MAY PLAY A ROLE IN THE NERVOUS SYSTEM AND IN THE
 CC REGULATION OF BEATING FREQUENCY IN PACEMAKER CELLS.
 CC -!- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=PI7971-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=PI7971-2; Sequence=Not described;
 CC -!- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -!- MISCELLANEOUS: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND
 CC IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -!- SIMILARITY: BELONGS TO THE POTASSIUM CHANNEL FAMILY. SHAL
 CC SUBFAMILY.
 CC -!- CAUTION: Ref.3 sequence differs from that shown due to erroneous
 CC gene model prediction.

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DR EMBL; M32660; AAA28895.1; -.
 DR EMBL; AE003516; AAF49144.1; ALT_SEQ.
 DR PIR; A35312; A35312.
 DR FlyBase; FBgn0005564; Shal.
 DR InterPro; IPR000210; BTB_POZ.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR001622; K+channel_pore.
 DR InterPro; IPR003091; K_channel.
 DR InterPro; IPR003131; K_tetra.
 DR InterPro; IPR003968; Kv_channel.
 DR InterPro; IPR005820; M+channel_nlg.
 DR InterPro; IPR003975; Shal_channel.
 DR Pfam; PF00520; ion_trans; 1.
 DR Pfam; PF02214; K_tetra; 1.
 DR PRINTS; PR00169; KCHANNEL.
 DR PRINTS; PR01491; KVCHANNEL.
 DR PRINTS; PR01497; SHALCHANNEL.
 DR SMART; SM00225; BTB; 1.

KW Transport; Ion transport; Ionic channel; Voltage-gated channel;
 KW Potassium channel; Potassium transport; Potassium; Transmembrane;
 KW Glycoprotein; Multigene family; Alternative splicing.

FT TRANSMEM 186 204 SEGMENT S1.
 FT TRANSMEM 229 250 SEGMENT S2.
 FT TRANSMEM 261 282 SEGMENT S3.

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FT   TRANSMEM   290   308   SEGMENT S4.
FT   TRANSMEM   324   345   SEGMENT S5.
FT   TRANSMEM   385   406   SEGMENT S6.
FT   CARBOHYD    46    46   N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   350   350   N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   353   353   N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   408   408   N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   490 AA;  55918 MW;  E178E1C89B07DA74 CRC64;

```

Query Match 4.6%; Score 104; DB 1; Length 490;

Best Local Similarity 27.7%; Pred. No. 1.2;

Matches 36; Conservative 27; Mismatches 41; Indels 26; Gaps 7;

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Qy      25 EVVELNVGGQVYFTRHSTLISIPHSLWKMFSPKRDTANDLAKDSKGRFFIDRDGFLFRY 84
      | : :|| | : : | :|| | :|| | :| | :| ||| :||:
Db      41 EKLLINVSGRRFETWRNTLEKYPDTLLG---SNEREFFYD--EDCK-EYFFDRDPDIFRH 94

Qy      85 ILDYLRDRQVVLDPHFPEKGRL---KREAEYFQ-LPDLVKLLTPDEIKQSPDEFCHSDFE 140
      ||:| | :: | :| | | :| :||:: : | : | :
Db      95 ILNYYRTGKL-----HYPKHECLTSYDEELAFFGIMPdVI-----GDCCYEDYR 138

Qy      141 DASQGSdTRI 150
      | : : | :
Db      139 DRKRENAERL 148

```

RESULT 6

YR43_CAEEL

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ID   YR43_CAEEL      STANDARD;          PRT;   140 AA.
AC   Q09389;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hypothetical 16.3 kDa protein F47D12.3 in chromosome III.
GN   F47D12.3.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Taich A.;
RL   Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.

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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----
DR   EMBL; U22831; AAK20065.1; -.
DR   PIR; A88479; A88479.
DR   WormPep; F47D12.3; CE01947.
DR   InterPro; IPR003131; K_tetra.

```

DR Pfam; PF02214; K_tetra; 1.
KW Hypothetical protein.
SQ SEQUENCE 140 AA; 16301 MW; E4866BD5F2A6CA15 CRC64;

Query Match 4.5%; Score 103.5; DB 1; Length 140;
Best Local Similarity 27.3%; Pred. No. 0.25;
Matches 42; Conservative 24; Mismatches 55; Indels 33; Gaps 5;

```
Qy      3 LSGNCSRYYPREQGSAVPNSFPEVVVELNVGGQVYFTRHSTL-----ISIPHS 49
          || || : : | |||::| : || : : :
Db      5 LSFNCEDAW-----LNLFGGEMYPVQVKTLMNPTTCGSYFRDVVKVSDA 49

Qy     50 LLWKMFSFKRDTANDLAKDSKGRFFIDRDGFLFRYILDYLRDRQVV-LPDHFFPEKGRLKR 108
          : |: : ||| | | |||| |||::| |||: :: ||| |
Db     50 AI-KVRGVQWDTA---PNHIKFRVDIDRDGVLFRHVLQYLRNGKLTSLPDDIFTLESIVA 105

Qy    109 EAEYFQLPDLVKLLTPDEIKQSPDEFCHSDFEDA 142
          |||:| | :| | : : :||:
Db    106 EAEFFGLEKYREMLKKKLWKLTGKRQYYACYEDS 139
```

RESULT 7

KCS3_RAT

ID KCS3_RAT STANDARD; PRT; 491 AA.
AC O88759; O54900;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Potassium voltage-gated channel subfamily S member 3 (Potassium
DE channel Kv9.3) (Delayed-rectifier K+ channel alpha subunit 3).
GN KCNS3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, and Kidney;
RX MEDLINE=98031889; PubMed=9362476;
RA Patel A.J., Lazdunski M., Honore E.;
RT "Kv2.1/Kv9.3, a novel ATP-dependent delayed-rectifier K+ channel in
RT oxygen-sensitive pulmonary artery myocytes.";
RL EMBO J. 16:6615-6625(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98369652; PubMed=9704029;
RA Stocker M., Kerschensteiner D.;
RT "Cloning and tissue distribution of two new potassium channel
RT alpha-subunits cloned from rat brain.";
RL Biochem. Biophys. Res. Commun. 248:927-934(1998).
CC -!- FUNCTION: Potassium channel subunit. Modulates channel activity
CC and shifts the activation threshold of KCNB1 to more negative
CC values.
CC -!- SUBUNIT: Heteromultimer with KCNB1 and with KCNB2. Does not form
CC homomultimers. Might also bind to other channel proteins (By
CC similarity).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein. May not reach the
 CC plasma membrane but remain in an intracellular compartment in the
 CC absence of KCNB1 (By similarity).
 CC -!- TISSUE SPECIFICITY: Detected in lung, spleen, brain and heart.
 CC -!- DOMAIN: The segment S4 is probably the voltage-sensor and is
 CC characterized by a series of positively charged amino acids at
 CC every third position.
 CC -!- MISCELLANEOUS: Inhibited by 4-aminopyridine (4-AP). Channel
 CC activity is reversibly inhibited by hypoxia and down-regulated in
 CC the absence of intracellular ATP.
 CC -!- SIMILARITY: BELONGS TO THE POTASSIUM CHANNEL FAMILY. S SUBFAMILY.

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DR EMBL; AF029056; AAB94882.1; -.
 DR EMBL; Y17607; CAA76805.1; -.
 DR InterPro; IPR000210; BTB_POZ.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR001622; K+channel_pore.
 DR InterPro; IPR003091; K_channel.
 DR InterPro; IPR003131; K_tetra.
 DR InterPro; IPR003971; Kv9_channel.
 DR InterPro; IPR003968; Kv_channel.
 DR InterPro; IPR005820; M+channel_nlg.
 DR Pfam; PF00520; ion_trans; 1.
 DR Pfam; PF02214; K_tetra; 1.
 DR PRINTS; PR00169; KCHANNEL.
 DR PRINTS; PR01494; KV9CHANNEL.
 DR PRINTS; PR01491; KVCHANNEL.
 DR SMART; SM00225; BTB; 1.

KW Transport; Ion transport; Ionic channel; Voltage-gated channel;
 KW Potassium channel; Potassium; Potassium transport; Transmembrane;
 KW Multigene family.

FT	DOMAIN	1	185	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	186	206	SEGMENT S1 (POTENTIAL).
FT	TRANSMEM	224	244	SEGMENT S2 (POTENTIAL).
FT	DOMAIN	245	253	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	254	274	SEGMENT S3 (POTENTIAL).
FT	TRANSMEM	288	308	SEGMENT S4 (POTENTIAL).
FT	DOMAIN	309	323	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	324	344	SEGMENT S5 (POTENTIAL).
FT	DOMAIN	358	378	SEGMENT H5 (PORE-FORMING) (POTENTIAL).
FT	TRANSMEM	385	405	SEGMENT S6 (POTENTIAL).
FT	DOMAIN	406	491	CYTOPLASMIC (POTENTIAL).
FT	CONFLICT	113	113	I -> F (IN REF. 1).
SQ	SEQUENCE	491 AA;	55865 MW;	6157BC7EFE94CC2B CRC64;

Query Match 4.5%; Score 102; DB 1; Length 491;
 Best Local Similarity 25.9%; Pred. No. 1.7;
 Matches 35; Conservative 25; Mismatches 51; Indels 24; Gaps 5;

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Qy      20  PNSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSFKRDTA-----NDLAKDSKGRFF 74
      |   |:| |||||      |||: ||: | |: :   :|   :| :   | ::
Db      10  PGQDEELVNLNVGGFKQSVQSTLLRFPHTRLGKLLTCHSEEAILELCDDYSVADK-EYY 68

Qy      75  IDRDGFLFRYILDYLRDRQVVLDPHFPEK---GRLKREAEYFQLPDLVKLLTPDEIKQSP 131
      ||: ||||:|::   ::   | |:   :| ||: : :|
Db      69  FDRNPSLFRYVLNFYYTGKL----HVMEELCVFSFCQEIEYWGINELF-----I 113

Qy     132  DEFCHSDFEDASQGS 146
      | | | :: : |
Db     114  DSCCSSRYQERKEES 128

```

RESULT 8

DNM1_CHICK

```

ID   DNM1_CHICK      STANDARD;          PRT;   1537 AA.
AC   Q92072;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   DNA (cytosine-5)-methyltransferase 1 (EC 2.1.1.37) (Dnmt1) (DNA
DE   methyltransferase GgaI) (DNA MTase GgaI) (MCMT) (M.GgaI).
GN   DNMT1 OR DNMT OR AIM.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96172572; PubMed=8586618;
RA   Tajima S., Tsuda H., Wakabayashi N., Asaso A., Mizuno S.,
RA   Nishimori K.;
RT   "Isolation and expression of a chicken DNA methyltransferase cDNA.";
RL   J. Biochem. 117:1050-1057(1995).
RN   [2]
RP   INTERACTION WITH PCNA, AND MUTAGENESIS OF VAL-190.
RX   MEDLINE=97451025; PubMed=9302295;
RA   Chuang L.S.-H., Ian H.-I., Koh T.-W., Ng H.-H., Xu G., Li B.F.L.;
RT   "Human DNA-(cytosine-5) methyltransferase-PCNA complex as a target for
RT   p21WAF1.";
RL   Science 277:1996-2000(1997).
CC   -!- FUNCTION: Methylates CpG residues. Preferentially methylates
CC   hemimethylated DNA. It is responsible for maintaining methylation
CC   patterns established in development (By similarity). Mediates
CC   transcriptional repression by direct binding to HDAC2 (By
CC   similarity).
CC   -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + DNA = S-adenosyl-L-
CC   homocysteine + DNA containing 5-methylcytosine.
CC   -!- SUBUNIT: Interacts with PCNA.
CC   -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC   -!- TISSUE SPECIFICITY: Testis and lung.
CC   -!- SIMILARITY: BELONGS TO THE C5-METHYLTRANSFERASE FAMILY.
CC   -!- SIMILARITY: Contains 2 BAH domains.
CC   -!- SIMILARITY: Contains 1 CXXC-type zinc finger.
CC   -----
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DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Potassium voltage-gated channel subfamily S member 3 (Potassium
 DE channel Kv9.3) (Delayed-rectifier K⁺ channel alpha subunit 3).
 GN KCNS3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND VARIANT THR-450.
 RC TISSUE=Lens epithelium;
 RX MEDLINE=99413882; PubMed=10484328;
 RA Shepard A.R., Rae J.L.;
 RT "Electrically silent potassium channel subunits from human lens
 RT epithelium.";
 RL Am. J. Physiol. 277:C412-C424(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney, and Skin;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Potassium channel subunit. Modulates channel activity
 CC and reduces the ion flow (By similarity).
 CC -!- SUBUNIT: Heteromultimer with KCNB1 and with KCNB2. Does not form
 CC homomultimers. Might also bind to other channel proteins (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. May not reach the
 CC plasma membrane but remain in an intracellular compartment in the
 CC absence of KCNB1.
 CC -!- TISSUE SPECIFICITY: Detected in most tissues, but not in
 CC peripheral blood lymphocytes. The highest levels of expression are
 CC in lung.
 CC -!- DOMAIN: The segment S4 is probably the voltage-sensor and is
 CC characterized by a series of positively charged amino acids at
 CC every third position.
 CC -!- SIMILARITY: BELONGS TO THE POTASSIUM CHANNEL FAMILY. S SUBFAMILY.

```

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CC -----
DR EMBL; AF043472; AAC13164.1; -.
DR EMBL; BC004148; AAH04148.1; -.
DR EMBL; BC004987; AAH04987.1; -.
DR EMBL; BC015947; AAH15947.1; -.
DR Genew; HGNC:6302; KCNS3.
DR MIM; 603888; -.
DR InterPro; IPR000210; BTB_POZ.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003091; K_channel.
DR InterPro; IPR003131; K_tetra.
DR InterPro; IPR003971; Kv9_channel.
DR InterPro; IPR003968; Kv_channel.
DR InterPro; IPR005820; M+channel_nlg.
DR Pfam; PF00520; ion_trans; 1.
DR Pfam; PF02214; K_tetra; 1.
DR PRINTS; PR00169; KCHANNEL.
DR PRINTS; PR01494; KV9CHANNEL.
DR PRINTS; PR01491; KVCHANNEL.
DR SMART; SM00225; BTB; 1.
KW Transport; Ion transport; Ionic channel; Voltage-gated channel;
KW Potassium channel; Potassium; Potassium transport; Transmembrane;
KW Multigene family; Polymorphism.
FT DOMAIN 1 185 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 186 206 SEGMENT S1 (POTENTIAL).
FT TRANSMEM 219 239 SEGMENT S2 (POTENTIAL).
FT DOMAIN 240 253 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 254 274 SEGMENT S3 (POTENTIAL).
FT TRANSMEM 288 308 SEGMENT S4 (POTENTIAL).
FT DOMAIN 309 323 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 324 344 SEGMENT S5 (POTENTIAL).
FT DOMAIN 358 378 SEGMENT H5 (PORE-FORMING) (POTENTIAL).
FT TRANSMEM 386 406 SEGMENT S6 (POTENTIAL).
FT DOMAIN 407 491 CYTOPLASMIC (POTENTIAL).
FT VARIANT 450 450 A -> T.
FT /FTid=VAR_014200.
FT CONFLICT 27 27 S -> Y (IN REF. 2; AAH15947).
FT CONFLICT 225 225 L -> V (IN REF. 1 AND 2; AAH15947).
SQ SEQUENCE 491 AA; 55984 MW; A5F12BF077A50DAD CRC64;

Query Match 4.4%; Score 100; DB 1; Length 491;
Best Local Similarity 25.4%; Pred. No. 2.5;
Matches 35; Conservative 28; Mismatches 61; Indels 14; Gaps 5;

Qy 20 PNSFPEVVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTA-----NDLAKDSKGRFF 74
| :| ||||| |||: ||: | |: : :| :| : | ::
Db 10 PGQDEELVNLNVGGFKQSVQSTLLRFPHTRLGKLLTCHSEEAILCDDYSVADK-EYY 68

```

Qy 75 IDR DGFLFRYILDYLRDRQVVLDPHFPEK---GRLKREA EYFQLPDL-VKLLTPDEIKQS 130
 ||: |||:|:: : : | | : : | ||: : : | : : :
 Db 69 FDRNPSLFRYVLNFYYTGKL----HVMEELCVFSFCQEIEYWGINELFIDSCCSNRYQER 124

Qy 131 PDEFCHSDFEDASQGS DT 148
 :| |:: | |
 Db 125 KEENHEKDWDQKSHDVST 142

RESULT 10

ADDA_HUMAN

ID ADDA_HUMAN STANDARD; PRT; 737 AA.
 AC P35611; Q13734; Q14729; Q16156; Q9UJB6;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Alpha adducin (Erythrocyte adducin alpha subunit).
 GN ADD1 OR ADDA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., SEQUENCE OF 24-36; 41-47; 516-569 AND 722-729, AND
 RP VARIANT CYS-586.
 RC TISSUE=Reticulocytes;
 RX MEDLINE=92011907; PubMed=1840603;
 RA Joshi R.L., Gilligan D.M., Otto E., McLaughlin T., Bennett V.D.;
 RT "Primary structure and domain organization of human alpha and beta
 RT adducin.";
 RL J. Cell Biol. 115:665-675(1991).
 RN [2]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RX MEDLINE=95293415; PubMed=7774961;
 RA Lin B., Nasir J., McDonald H., Graham R., Rommens J.M., Goldberg Y.P.,
 RA Hayden M.R.;
 RT "Genomic organization of the human alpha-adducin gene and its
 RT alternately spliced isoforms.";
 RL Genomics 25:93-99(1995).
 RN [3]
 RP SEQUENCE OF 121-170 FROM N.A.
 RA Hall C.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE OF 171-737 FROM N.A.
 RA Mungall A.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
 RN [5]
 RP SEQUENCE OF 531-737 FROM N.A.
 RX MEDLINE=94258208; PubMed=1345173;
 RA Taylor S.A., Snell R.G., Buckler A., Ambrose C., Duyao M.,
 RA Church D., Lin C.S., Altherr M., Bates G.P., Groot N.;
 RT "Cloning of the alpha-adducin gene from the Huntington's disease
 RT candidate region of chromosome 4 by exon amplification.";
 RL Nat. Genet. 2:223-227(1992).
 RN [6]
 RP PHOSPHORYLATION SITES, AND PARTIAL SEQUENCE.

RX MEDLINE=96411719; PubMed=8810272;
 RA Matsuoka Y., Hughes C.A., Bennett V.;
 RT "Adducin regulation. Definition of the calmodulin-binding domain and
 RT sites of phosphorylation by protein kinases A and C.";
 RL J. Biol. Chem. 271:25157-25166(1996).
 RN [7]
 RP VARIANT TRP-460.
 RX MEDLINE=98337407; PubMed=9674650;
 RA Kamitani A., Wong Z.Y., Fraser R., Davies D.L., Connor J.M., Foy C.J.,
 RA Watt G.C., Harrap S.B.;
 RT "Human alpha-adducin gene, blood pressure, and sodium metabolism.";
 RL Hypertension 32:138-143(1998).
 RN [8]
 RP VARIANTS TRP-460 AND CYS-586.
 RX MEDLINE=99318094; PubMed=10391210;
 RA Halushka M.K., Fan J.-B., Bentley K., Hsie L., Shen N., Weder A.,
 RA Cooper R., Lipshutz R., Chakravarti A.;
 RT "Patterns of single-nucleotide polymorphisms in candidate genes for
 RT blood-pressure homeostasis.";
 RL Nat. Genet. 22:239-247(1999).
 CC -!- FUNCTION: MEMBRANE-CYTOSKELETON-ASSOCIATED PROTEIN THAT PROMOTES
 CC THE ASSEMBLY OF THE SPECTRIN-ACTIN NETWORK. BINDS TO CALMODULIN.
 CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT OR AN ALPHA
 CC AND A GAMMA SUBUNIT.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Comment=Additional isoforms seem to exist;
 CC Name=1;
 CC IsoId=P35611-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P35611-2; Sequence=VSP_000175, VSP_000176;
 CC Name=3;
 CC IsoId=P35611-3; Sequence=VSP_000174;
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES. FOUND IN MUCH HIGHER
 CC LEVELS IN RETICULOCYTES THAN THE BETA SUBUNIT.
 CC -!- DOMAIN: EACH SUBUNIT IS COMPRISED OF THREE REGIONS: A NH2-TERMINAL
 CC PROTEASE-RESISTANT GLOBULAR HEAD REGION, A SHORT CONNECTING
 CC SUBDOMAIN, AND A PROTEASE-SENSITIVE TAIL REGION.
 CC -!- PTM: THE N-TERMINUS IS BLOCKED.
 CC -!- SIMILARITY: BELONGS TO THE ALDOLASE CLASS II FAMILY. ADDUCIN
 CC SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL; X58141; CAA41149.1; -.
 DR EMBL; L29296; AAB05645.1; -.
 DR EMBL; L29286; AAB05645.1; JOINED.
 DR EMBL; L29287; AAB05645.1; JOINED.
 DR EMBL; L29289; AAB05645.1; JOINED.
 DR EMBL; L29290; AAB05645.1; JOINED.
 DR EMBL; L29291; AAB05645.1; JOINED.

DR EMBL; L29292; AAB05645.1; JOINED.
 DR EMBL; L29293; AAB05645.1; JOINED.
 DR EMBL; L29294; AAB05645.1; JOINED.
 DR EMBL; L29295; AAB05645.1; JOINED.
 DR EMBL; L29297; AAB05645.1; JOINED.
 DR EMBL; L29298; AAB05645.1; JOINED.
 DR EMBL; Z74617; CAA98970.1; -.
 DR EMBL; Z68280; CAA92578.1; -.
 DR EMBL; S70314; AAB30914.2; -.
 DR PIR; S18207; S18207.
 DR Genew; HGNC:243; ADD1.
 DR MIM; 102680; -.
 DR GO; GO:0003779; F:actin binding activity; TAS.
 DR InterPro; IPR001303; Aldolase_II_N.
 DR Pfam; PF00596; Aldolase_II; 1.
 KW Cytoskeleton; Membrane; Calmodulin-binding; Phosphorylation;
 KW Alternative splicing; Polymorphism.
 FT DOMAIN 717 734 CALMODULIN-BINDING (POTENTIAL).
 FT MOD_RES 59 59 PHOSPHORYLATION (BY PKA).
 FT MOD_RES 408 408 PHOSPHORYLATION (BY PKA).
 FT MOD_RES 436 436 PHOSPHORYLATION (BY PKA).
 FT MOD_RES 481 481 PHOSPHORYLATION (BY PKA).
 FT MOD_RES 716 716 PHOSPHORYLATION (BY PKC).
 FT MOD_RES 726 726 PHOSPHORYLATION (BY PKC AND PKA).
 FT VARSPLIC 471 471 K -> KVTNITHDHVKPLLQSLSSGVCVPSCITNCL (in
 FT isoform 3).
 FT /FTId=VSP_000174.
 FT VARSPLIC 621 631 DLVPEPTTGDD -> GDGCAREYLLP (in isoform
 FT 2).
 FT /FTId=VSP_000175.
 FT VARSPLIC 632 737 Missing (in isoform 2).
 FT /FTId=VSP_000176.
 FT VARIANT 270 270 Y -> N (in dbSNP:4971).
 FT /FTId=VAR_014863.
 FT VARIANT 376 376 E -> D (in dbSNP:4972).
 FT /FTId=VAR_014864.
 FT VARIANT 460 460 G -> W (in dbSNP:4961).
 FT /FTId=VAR_014184.
 FT VARIANT 510 510 N -> I (in dbSNP:4962).
 FT /FTId=VAR_014865.
 FT VARIANT 586 586 S -> C (in dbSNP:4963).
 FT /FTId=VAR_014185.
 FT CONFLICT 606 606 A -> E (IN REF. 2).
 SQ SEQUENCE 737 AA; 80955 MW; DF13AB30B12F20B6 CRC64;

Query Match 4.4%; Score 100; DB 1; Length 737;
 Best Local Similarity 18.6%; Pred. No. 4.3;
 Matches 95; Conservative 77; Mismatches 174; Indels 164; Gaps 24;

Qy 22 SFPEVVELNVGGQVYFTRHSTLIS-----IPHSLWKMFSPPKRDANDLAKDSKGRF 73
 :| : :| | : : :| :: :| ||: ||: | | :
 Db 151 AFYRLADLFWSQLIYNHITTRVNSEQEHFLIVPFGLLY-----SEVTASSLVKINLQGD 205
 Qy 74 FIDRD-----GFLFRYILDYLR-DRQVLPDHFPEKGRLEKREAEYFQLPDLVKLLT 123
 :|| || : | | : | : | | | : || ::
 Db 206 IVDRGSTNLGVNQAGFTLHSAIYAARPDVKCVVHIHTP-AGAAVSAMKCGLLP-----IS 259

Qy 124 PDEIKQSPDEFCHSD FEDASQGS DTRICPPSSLLPAD-----RKWGFITVGYRG SCTLGR 178
 | : : | | : | : : : : : | | | : : | |
 Db 260 PEAL--SLGEVAYHDYHGILVDEEEKVLIQKNLGP KSKVLILRNHGLVSVG----- 308

Qy 179 EGQADAKFRRVPRILVCGRISLAKEVFGETLINESRDPDRA----PERYTS----- 224
 : | : : : | | : | | : | | : | :
 Db 309 -ESVEEAFYYIHNLVV-----ACEIQVRTLASAGGPDNLVLLNPEKYKAKSRSPGSPVG 361

Qy 225 -----RFYLFKFKHLERAFDMLSECGFHM-VACNSSVTASFINQYTD DDKIWSSSYTEYVF 276
 : : : : | | | : : : : | : : : | | |
 Db 362 EGTGSPPKWQIGEQE FEALMRMLDNLGYRTGYPRYPALREKSKKYSDVEVPASVTGYSF 421

Qy 277 -----YREPSRWSPSHCDCCCKNGKGD---KEGESGTSCND----- 309
 | | : | | : | : | : | : | : | : | : |
 Db 422 ASDGDSGTCSPLRHSFQKQQREKTRW-----LNSGRGDEASEEQNGSSPKSKTKWT 473

Qy 310 -----LSTSSCDSQS-----EASSPQETVICGPVTRQTN 338
 | : | : : | : : | : | : | : | : | : |
 Db 474 KEDGHRTSTSAVPNLFVPLNTNPKEVQEMRNKIREQN LQDIKTAGPQSQVLCGVV----- 528

Qy 339 IQTLDRPIKKGFPVQLIQQSEM---RRKSDLLRIILTSG-----SRESNMSSKKKAVKE 387
 : | | : : | : | : | : : : | : | : | : : | :
 Db 529 ---MDRSLVQG--ELVTASKAIEKEYQPHVIVSTTGPNPFTT LTDRELEEYRREVERKQ 583

Qy 388 KLSIEEELEKCIQDFLKKKIPDRFPERKHP 417
 | | | | | : : : | : | | | | |
 Db 584 KGS-EENLDEAREQ--KEKSPPDQPAVPHP 610

RESULT 11

KCS3_RABIT

ID KCS3_RABIT STANDARD; PRT; 491 AA.
 AC Q9TT17;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Potassium voltage-gated channel subfamily S member 3 (Potassium
 DE channel Kv9.3) (Delayed-rectifier K+ channel alpha subunit 3).
 GN KCNS3.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=New Zealand white; TISSUE=Corneal epithelium;
 RA Rae J.L.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: Potassium channel subunit. Modulates channel activity
 CC and reduces the ion flow (By similarity).
 CC -!- SUBUNIT: Heteromultimer with KCNB1 and with KCNB2. Does not form
 CC homomultimers. Might also bind to other channel proteins (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. May not reach the
 CC plasma membrane but remain in an intracellular compartment in the
 CC absence of KCNB1 (By similarity).
 CC -!- DOMAIN: The segment S4 is probably the voltage-sensor and is

CC characterized by a series of positively charged amino acids at
 CC every third position.
 CC -!- SIMILARITY: BELONGS TO THE POTASSIUM CHANNEL FAMILY. S SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL; AF209723; AAF22833.1; -.
 DR InterPro; IPR000210; BTB_POZ.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR001622; K+channel_pore.
 DR InterPro; IPR003091; K_channel.
 DR InterPro; IPR003131; K_tetra.
 DR InterPro; IPR003971; Kv9_channel.
 DR InterPro; IPR003968; Kv_channel.
 DR InterPro; IPR005820; M+channel_nlg.
 DR Pfam; PF00520; ion_trans; 1.
 DR Pfam; PF02214; K_tetra; 1.
 DR PRINTS; PR00169; KCHANNEL.
 DR PRINTS; PR01494; KV9CHANNEL.
 DR PRINTS; PR01491; KVCHANNEL.
 DR SMART; SM00225; BTB; 1.
 KW Transport; Ion transport; Ionic channel; Voltage-gated channel;
 KW Potassium channel; Potassium; Potassium transport; Transmembrane;
 KW Multigene family.
 FT DOMAIN 1 185 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 186 206 SEGMENT S1 (POTENTIAL).
 FT TRANSMEM 224 244 SEGMENT S2 (POTENTIAL).
 FT DOMAIN 245 253 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 254 274 SEGMENT S3 (POTENTIAL).
 FT TRANSMEM 288 308 SEGMENT S4 (POTENTIAL).
 FT DOMAIN 309 323 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 324 344 SEGMENT S5 (POTENTIAL).
 FT DOMAIN 358 378 SEGMENT H5 (PORE-FORMING) (POTENTIAL).
 FT TRANSMEM 386 406 SEGMENT S6 (POTENTIAL).
 FT DOMAIN 407 491 CYTOPLASMIC (POTENTIAL).
 SQ SEQUENCE 491 AA; 55941 MW; 2EE396E0889D6F77 CRC64;

Query Match 4.3%; Score 99; DB 1; Length 491;
 Best Local Similarity 25.4%; Pred. No. 3;
 Matches 35; Conservative 28; Mismatches 61; Indels 14; Gaps 5;

Qy 20 P NSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFS PKRDTA-----NDLAKDSKGRFF 74
 | :| ||||| |||: ||: | |: : : | :| : | ::
 Db 10 PGPDEELVNLNVGGFKQSVDQSTLLRFP HTRLGKLLTCHSEEAILELCDDYSVADK-EYY 68
 Qy 75 I DRDGF LFRYILDYLRDRQVVL PDHFPEK---GR LKREA EYFQLPDL-VKLLTPDEIKQS 130
 ||: ||||:|:: : : | |: :| ||: : :| : : : :
 Db 69 FDRNP SLFRYVLNFYYTGKL----HVMEELCVFSFCQEIEYWG INELFIDSCCSNRYQER 124
 Qy 131 PDEFCHSDFEDASQGS DT 148
 :| |:: | |

RESULT 12

IRF1_MOUSE

ID IRF1_MOUSE STANDARD; PRT; 329 AA.
AC P15314;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Interferon regulatory factor 1 (IRF-1).
GN IRF1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88311092; PubMed=3409321;
RA Miyamoto M., Fujita T., Kimura Y., Maruyama M., Harada H.,
RA Sudo Y., Miyata T., Taniguchi T.;
RT "Regulated expression of a gene encoding a nuclear factor, IRF-1,
RT that specifically binds to IFN-beta gene regulatory elements.";
RL Cell 54:903-913(1988).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 7-111.
RX MEDLINE=98082978; PubMed=9422515;
RA Escalante C.R., Yie J., Thanos D., Aggarwal A.K.;
RT "Structure of IRF-1 with bound DNA reveals determinants of interferon
RT regulation.";
RL Nature 391:103-106(1998).
CC -!- FUNCTION: SPECIFICALLY BINDS TO THE UPSTREAM REGULATORY REGION
CC OF TYPE I IFN AND IFN-INDUCIBLE MHC CLASS I GENES (THE INTERFERON
CC CONSENSUS SEQUENCE (ICS)) AND ACTIVATES THOSE GENES.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- INDUCTION: By viruses and IFN.
CC -!- SIMILARITY: Belongs to the IRF family.
CC -----
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CC -----
DR EMBL; M21065; AAA39334.1; -.
DR PIR; A31595; A31595.
DR PDB; 1IF1; 25-FEB-98.
DR TRANSFAC; T00422; -.
DR MGD; MGI:96590; Irfl.
DR InterPro; IPR001346; IRF.
DR Pfam; PF00605; IRF; 1.
DR PRINTS; PR00267; INTERNREGFCT.
DR ProDom; PD002355; IRF; 1.
DR SMART; SM00348; IRF; 1.
DR PROSITE; PS00601; IRF; 1.

KW Transcription regulation; DNA-binding; Activator; Nuclear protein;
 KW Interferon induction; 3D-structure.
 FT DNA_BIND 7 109 TRYPTOPHAN PENTAD REPEAT.
 FT HELIX 12 20
 FT STRAND 33 34
 FT TURN 41 42
 FT TURN 44 45
 FT TURN 48 50
 FT HELIX 54 61
 FT TURN 62 63
 FT HELIX 74 87
 FT STRAND 91 93
 FT STRAND 107 109
 SQ SEQUENCE 329 AA; 37319 MW; 0E5DD23C0D977B34 CRC64;

Query Match 4.3%; Score 98; DB 1; Length 329;
 Best Local Similarity 20.1%; Pred. No. 2.1;
 Matches 69; Conservative 53; Mismatches 130; Indels 92; Gaps 16;

Qy 31 VGGQVYFTRHSTLISIPHSLLWKMFS PKRDTANDLAKDSKGRFFIDRDGFLFRYILDYLR 90
 : | :: : : || || : | : | :: | ||| : :
 Db 21 IPGLIWINKEEMIFQIP-----WK-----HAAKHGWDINKDACLFRSWAIHTG 63
 Qy 91 DRQVVLDPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQSPDEFCHSDFEDASQGSDT-- 148
 : : | : : ||| : : | : : : : : ||
 Db 64 RYKAGEKEPDPKTWKANFRFCAMNSLPDI-----EEVKD-----QSRNKGSSAVR 107
 Qy 149 --RICPPSSLLPADRKWGFITVGYRGSC TLGREGQADAKFRRVPRIILVCGRISLAKEVFG 206
 | : || | || | : : : : : : || : | : |
 Db 108 VYRMLPP--LTRNQRK-----ERKSKSSRDTSKTKRKLCGDVS--PD TFS 149
 Qy 207 ETLNESRDPDRAPERYTSRFY LKFH LERAFDM---LSEC-----GFHM----- 247
 : | : | || || : : || : | : | : || : ||
 Db 150 DGLSSSTLPD-DHSSYTTQGYLG-QDLDMERDITPALSPCVVSSSLSEWHMQMDIIPDST 207
 Qy 248 -----VACNSSVTASFINQYTD DDKIWSSYTEYVFYREPSRWSPSHCDCCCKNGKGDKE 300
 | : | : : : : || : | | | | : | | |||
 Db 208 TDLYNLQVSPMPSTSEAA TDEDEEGKIAEDLMKLF---EQSEWQPTHID-----GKG YLL 259
 Qy 301 GESGTSCNDL-STSSCDSQSEASSPQETVICGPVTRQTNIQTLD 343
 | || : : || : | || : : | | : : |
 Db 260 NEPGTQLSSVYGDFSCKEEPEIDSPRGDIGIGIQHVFTMKNM D 303

RESULT 13

SWI3_YEAST

ID SWI3_YEAST STANDARD; PRT; 825 AA.
 AC P32591;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Transcription regulatory protein SWI3 (SWI/SNF complex component SWI3)
 DE (Transcription factor TYE2).
 GN SWI3 OR TYE2 OR YJL176C OR J0495.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92154671; PubMed=1339306;
 RA Peterson C.L., Herskowitz I.;
 RT "Characterization of the yeast SWI1, SWI2, and SWI3 genes, which
 RT encode a global activator of transcription."
 RL Cell 68:573-583(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Loehning C., Mueller C., Freidel K., Ciriacy M.;
 RL Submitted (NOV-1990) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Obermaier B., Piravandi E., Rinke M., Domdey H.;
 RL Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: INVOLVED IN TRANSCRIPTIONAL ACTIVATION. THE SWI/SNF
 CC COMPLEX IS REQUIRED FOR THE INDUCED EXPRESSION OF A LARGE NUMBER
 CC OF GENES. THIS COMPLEX ALTERS CHROMATIN STRUCTURE TO FACILITATE
 CC BINDING OF GENE-SPECIFIC DEDICATED TRANSCRIPTION FACTORS.
 CC INTERACTS WITH THE N-TERMINUS OF SNF2.
 CC -!- SUBUNIT: COMPONENT OF THE SWI/SNF GLOBAL TRANSCRIPTION ACTIVATOR
 CC COMPLEX.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: Contains 1 Myb-like domain.
 CC -----
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 CC -----
 DR EMBL; M84390; AAA35136.1; -.
 DR EMBL; X56792; CAA40112.1; -.
 DR EMBL; Z49451; CAA89470.1; -.
 DR PIR; S26706; S26706.
 DR TRANSFAC; T02400; -.
 DR SGD; S0003712; SWI3.
 DR InterPro; IPR001005; Myb_DNA_binding.
 DR Pfam; PF00249; myb_DNA-binding; 1.
 DR Pfam; PF04433; SWIRM; 1.
 DR SMART; SM00717; SANT; 1.
 DR PROSITE; PS00037; MYB_1; FALSE_NEG.
 DR PROSITE; PS00334; MYB_2; FALSE_NEG.
 DR PROSITE; PS50090; MYB_3; 1.
 KW Transcription regulation; Activator; DNA-binding; Nuclear protein.
 FT DNA_BIND 526 569 MYB.
 FT DOMAIN 1 304 ASP/GLU-RICH (ACIDIC).
 FT DOMAIN 694 722 LEUCINE-ZIPPER.
 SQ SEQUENCE 825 AA; 92926 MW; DBA2E2022F15F9A6 CRC64;

Query Match 4.3%; Score 98; DB 1; Length 825;
 Best Local Similarity 24.4%; Pred. No. 7.1;
 Matches 85; Conservative 49; Mismatches 136; Indels 78; Gaps 21;

Qy 95 VLPDHF-----PEKGR LKR-EAEYFQLPDLVKLLTPDEIKQSPDEFCHS-DFEDASQGS DT 148
 :: || :| : | | | :| : : | | : : :
 Db 274 IMNDH SKSANPKKTTITRVEPETFEIPQAHEIVIPSYSKWFENLEKIHSIEVQSLPEFFTN 333

Qy 149 RICPPSSLLPADRKW-GFITVGYR-----GSCTLGR---EGQADAKFRRVPRILVCGRI 198
 || || : : | : || | | | | | | : | |
 Db 334 RI--PSKTPEVYMRYRNFMVNSYRLNPNEYFSVTTARRNVSGDAAALFRLHKFLTKWGLI 391

Qy 199 SLAKEVFGETLINESRDPDRAPERYTSRF-----YLKFKHLERAFDMLSECGFHMVAC 250
 : :| : | : :| : :| : :| : ||
 Db 392 NY--QVDSKLLPKNIEPP-LTSQYSTRHDAPRGLFPFESYKPSVQLPDM----- 437

Qy 251 NSSVTASFINQYTDKDWSSYTEYVFYREPSR-----WSPSHCDCCCKNGKGDKEGESG 304
 : :| | | | | : :| | | | : || |
 Db 438 --AKLKKMMN--TSD---SESTLYKYLKESKRKYDEITHPPSTTD----DENGDKNDNGG 486

Qy 305 TSCNDLSTSSCDSQSEASSPQETVICGPVTRQTNIQTLDRPIKKGFPVQLIQQ-SEMR RKS 363
 | : || | : | : | || :| : : :| | |
 Db 487 KMNNEVSTS-----TSMTGDANLLEEGET-SRPLKK--VKILEQIDENWSKE 530

Qy 364 DLLRILTS GSRNSMSSKKKAVKEKLSIEEELEKCIQDFLKKKIPDRF 411
 || : :| | :| | | : :| | : | :|
 Db 531 DLQKLL-KGIQEF GADWYKVA---KNVGNKSPEQCILRFLQLPIEDKF 574

RESULT 14

FMN_CHICK

ID FMN_CHICK STANDARD; PRT; 1213 AA.
 AC Q05858;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Formin (Limb deformity protein).
 GN LD.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=White leghorn; TISSUE=Embryo;
 RX MEDLINE=92112031; PubMed=1730407;
 RA Trumpp A., Blundell P.A., de la Pompa J.L., Zeller R.;
 RT "The chicken limb deformity gene encodes nuclear proteins expressed
 RT in specific cell types during morphogenesis.";
 RL Genes Dev. 6:14-28(1992).
 CC -!- FUNCTION: IS IMPORTANT FOR MORPHOGENESIS OF LIMB AND KIDNEY AND
 CC MAY BE INVOLVED IN DETERMINING DORSOVENTRAL NEURAL TUBE POLARITY
 CC AND MOTOR NEURON INDUCTION. IT MAY ALSO HAVE A FUNCTION IN
 CC DIFFERENTIATED CELLS OR BE INVOLVED IN MAINTAINING SPECIFIC
 CC DIFFERENTIATED STATES.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=1;
 CC Comment=A number of isoforms are produced;
 CC Name=1;

```

CC      IsoId=Q05858-1; Sequence=Displayed;
CC      -!- TISSUE SPECIFICITY: PRESENT IN THE ADULT BRAIN, KIDNEY, BRAIN,
CC      HEART AND INTESTINE AND THROUGHOUT THE EMBRYO.
CC      -!- DEVELOPMENTAL STAGE: IN THE DEVELOPING LIMB BUD, THE PROTEIN IS
CC      EXPRESSED IN THE APICAL ECTODERMAL RIDGE AND THE MESENCHYMAL
CC      COMPARTMENT, PREDOMINANTLY IN THE POSTERIOR REGION. DURING KIDNEY
CC      MORPHOGENESIS, EXPRESSION IS INITIALLY RESTRICTED TO THE
CC      EPITHELIAL COMPARTMENT OF THE PRONEPHROS AND MESONEPHROS.
CC      -!- SIMILARITY: Contains 1 Formin homology 1 (FH1) domain.
CC      -!- SIMILARITY: Contains 1 Formin homology 2 (FH2) domain.
CC      -!- SIMILARITY: BELONGS TO THE FORMIN HOMOLOGY FAMILY. CAPPUCCINO
CC      SUBFAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; X62681; CAA44555.1; -.
DR      PIR; S24286; A41724.
DR      InterPro; IPR003104; FH2.
DR      InterPro; IPR001265; Formin.
DR      Pfam; PF02181; FH2; 1.
DR      PRINTS; PR00828; FORMIN.
DR      SMART; SM00498; FH2; 1.
KW      Nuclear protein; Developmental protein; Coiled coil;
KW      Alternative splicing.
FT      DOMAIN      428      450      COILED COIL (POTENTIAL).
FT      DOMAIN      503      572      COILED COIL (POTENTIAL).
FT      DOMAIN      652      751      FH1 (PRO-RICH).
FT      DOMAIN      766      1171     FH2.
FT      DOMAIN      1050     1125     COILED COIL (POTENTIAL).
SQ      SEQUENCE    1213 AA;  135240 MW;  ADE3EF0B3FB9D862 CRC64;

      Query Match          4.3%;  Score 97.5;  DB 1;  Length 1213;
      Best Local Similarity 21.4%;  Pred. No. 13;
      Matches 104;  Conservative 50;  Mismatches 168;  Indels 165;  Gaps 23;

Qy      4  SGNCSRYYPREQSAVPNSFPEVVVELNVGGQVYFTRHS--TLISIPHSL-----L 51
      :  |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      5  NAGCSRQLPERAGPA--ESEP DV-----FTTFAVRTLLGLTTKLESVTPKEEEAV 52

Qy      52  WKMFSPKRDTANDLAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLDPDHFPEKGRLKREAE 111
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      53  LKAFQPLHIDVNTQANNRYER--NDNDGV----- 79

Qy      112 YFQLPDLVKLLTPDEIKQSPDEFCHSD FEDASQGS DTRICPPSSLLPADRKWGFITVGYR 171
      |  :  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      80  -----DDSENQHCESCTSDQADPM S GS--RAEPELEPEPAGQN-EILLPHLR 123

Qy      172 GSCTLGREGQADAKFRRVPRIILVCGRISLAKEVFGETL NESRDPDRAPER YTSRFY LKFK 231
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      124 SVQTSLS ESDNDA-----ILVQGT L-VHTTSDTESDGESKDPD-ADETGT SK----- 168

```

Qy 232 HLERAFDMLSECGFHMVACNSSVTASFINQ-----YTDDKIWSSYTEYVFYREP 280
 || : | |:| || ::|| : || :
 Db 169 -----CGLNNAAL-SAVALDGNNQSKEESDSEGYGHSDDTVGRDDTE--LHPPI 214
 Qy 281 SRWSPSHCDCCCKNGKGDKEGESGTSCND-----LSTSSCDSQ----- 318
 |:| | | :: | |: | :: |:| | :
 Db 215 SQWLPRKLD SILEH---DSSGKDRTLMDQFSCLLATGECSPELSGEDQRP SADNV SFHK 271
 Qy 319 ---SEASSPQETVICGPVTRQTNIQTLD-----RPIKKG PVQLIQQSEMRRKSDLLRI 368
 :| | | |: : | | :| :: : |: : :|:|
 Db 272 AALTERSFQLPAFFSGLRVRKKGLNTEDGETITEIKP-RENDLALLKLRQPVKKSN----- 326
 Qy 369 LTSGSRESNMSSKKKA---VKEKLS-----IEEELEKCIQDFLKKKIPDRFPERKH 416
 :||| ||: || |:| :| : | : : | || |
 Db 327 ITSGLTTKKKSSEPKASPTFLEQLSHLLNIDVSKNDERTQDSGAGFGETEDSDEGPENKA 386
 Qy 417 PWQSELL 423
 |:| |
 Db 387 SGQTEPL 393

RESULT 15

PKCB_HUMAN

ID PKCB_HUMAN STANDARD; PRT; 1186 AA.
 AC Q9ULU4; Q13517; Q8WXC5; Q9H1F3; Q9H1F4; Q9H1F5; Q9H1L8; Q9H1L9;
 AC Q9H2G5; Q9NYN3; Q9UIX6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Protein kinase C binding protein 1 (Rack7) (Cutaneous T-cell lymphoma
 DE associated antigen sel4-3) (CTCL tumor antigen sel4-3) (Zinc finger
 DE MYND domain containing protein 8).
 GN PRKCBP1 OR RACK7 OR ZMYND8 OR KIAA1125.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Hippocampus;
 RX MEDLINE=20458872; PubMed=11003709;
 RA Fossey S.C., Kuroda S., Price J.A., Pendleton J.K., Freedman B.I.,
 RA Bowden D.W.;
 RT "Identification and characterization of PRKCBP1, a candidate RACK-like
 RT protein.";
 RL Mamm. Genome 11:919-925(2000).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 3 AND 4).
 RC TISSUE=Testis;
 RX MEDLINE=21143360; PubMed=11149944;
 RA Eichmueller S., Usener D., Dummer R., Stein A., Thiel D.,
 RA Schadendorf D.;
 RT "Serological detection of cutaneous T-cell lymphoma-associated
 RT antigens.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:629-634(2001).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Brain;
 RX MEDLINE=20039618; PubMed=10574461;
 RA Hirose M., Nagase T., Ishikawa K.-I., Kikuno R., Nomura N.,
 RA Ohara O.;
 RT "Characterization of cDNA clones selected by the GeneMark analysis
 RT from size-fractionated cDNA libraries from human brain.";
 RL DNA Res. 6:329-336(1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Copley V.E., Collier R.E., Connor R., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Lehtvaslainen M.H., Liversidge M., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConnell L.J., McLay K., McMurray A.A.,
 RA Milne S., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 6).
 RC TISSUE=Eye;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzyzanski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- SUBUNIT: Interacts in vitro with PRKCB1.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=6;
 CC Comment=Experimental confirmation may be lacking for some
 CC isoforms;
 CC Name=1;
 CC IsoId=Q9ULU4-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9ULU4-2; Sequence=VSP_000566, VSP_000569;
 CC Name=3;
 CC IsoId=Q9ULU4-3; Sequence=VSP_000564, VSP_000568;
 CC Name=4;
 CC IsoId=Q9ULU4-4; Sequence=VSP_000565, VSP_000568;
 CC Name=5;
 CC IsoId=Q9ULU4-5; Sequence=VSP_000563, VSP_000567;
 CC Name=6;
 CC IsoId=Q9ULU4-6; Sequence=VSP_000564, VSP_000568, VSP_000570;
 CC -!- TISSUE SPECIFICITY: Expressed in all tissues examined with highest
 CC expression in brain, lung, pancreas, and placenta. Expressed in
 CC cutaneous T-cell lymphomas (CTCL).
 CC -!- SIMILARITY: Contains 1 bromodomain.
 CC -!- SIMILARITY: Contains 1 PHD-type zinc finger.
 CC -!- SIMILARITY: Contains 1 PWWP domain.
 CC -!- SIMILARITY: Contains 1 MYND-type zinc finger.
 CC -!- CAUTION: Ref.1 (AAC72244) sequence differs from that shown due to
 CC a frameshift in position 816.
 CC -!- CAUTION: Ref.4 sequence differs from that shown due to erroneous
 CC gene model prediction.
 CC -----
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 CC -----
 DR EMBL; AF233453; AAF71262.1; -.
 DR EMBL; U48251; AAC72244.1; ALT_FRAME.
 DR EMBL; AF454056; AAL50790.1; -.
 DR EMBL; AF273045; AAG34905.1; -.
 DR EMBL; AB032951; BAA86439.1; ALT_INIT.
 DR EMBL; AL031666; CAC19780.1; ALT_SEQ.
 DR EMBL; AL031666; CAC19781.1; ALT_TERM.
 DR EMBL; AL031666; CAC19782.1; ALT_TERM.
 DR EMBL; AL390212; CAC15980.2; ALT_INIT.
 DR EMBL; AL390212; CAC15981.1; ALT_SEQ.
 DR EMBL; AL049540; CAB56762.1; -.
 DR EMBL; BC030721; AAH30721.1; -.
 DR Genew; HGNC:9397; PRKCBP1.
 DR InterPro; IPR001487; Bromodomain.
 DR InterPro; IPR000313; PWWP_domain.
 DR InterPro; IPR002893; Znf_MYND.

DR InterPro; IPR001965; Znf_PHD.
DR Pfam; PF00439; bromodomain; 1.
DR Pfam; PF00628; PHD; 1.
DR Pfam; PF00855; PWWP; 1.
DR Pfam; PF01753; zf-MYND; 1.
DR PRINTS; PR00503; BROMODOMAIN.
DR SMART; SM00297; BROMO; 1.
DR SMART; SM00249; PHD; 1.
DR SMART; SM00293; PWWP; 1.
DR PROSITE; PS50014; BROMODOMAIN_2; 1.
DR PROSITE; PS50812; PWWP; 1.
DR PROSITE; PS01360; ZF_MYND_1; 1.
DR PROSITE; PS50865; ZF_MYND_2; 1.
DR PROSITE; PS01359; ZF_PHD_1; 1.
DR PROSITE; PS50016; ZF_PHD_2; 1.
KW Bromodomain; Zinc-finger; Alternative splicing.
FT ZN_FING 107 152 PHD-TYPE.
FT DOMAIN 184 254 BROMODOMAIN.
FT DOMAIN 296 346 PWWP.
FT ZN_FING 1028 1062 MYND-TYPE.
FT DOMAIN 1147 1186 INTERACTS WITH PRKCB1.
FT DOMAIN 43 47 POLY-LYS.
FT DOMAIN 838 854 POLY-GLN.
FT DOMAIN 1089 1092 POLY-SER.
FT VARSPLIC 1 1 M -> MHPQSLAEEEEIKTEQEVVEG (in isoform 5).
FT VARSPLIC 1 145 /FTId=VSP_000563.
FT VARSPLIC 1 145 Missing (in isoform 3 and isoform 6).
FT VARSPLIC 1 376 /FTId=VSP_000564.
FT VARSPLIC 1 376 Missing (in isoform 4).
FT VARSPLIC 1 526 /FTId=VSP_000565.
FT VARSPLIC 1 526 Missing (in isoform 2).
FT VARSPLIC 58 82 /FTId=VSP_000566.
FT VARSPLIC 58 82 Missing (in isoform 5).
FT VARSPLIC 823 869 /FTId=VSP_000567.
FT VARSPLIC 823 869 SKFQTSSQKWHMQKMRQQQQQQQNQQQQPQSSQGTRYQT
FT RQAVKA -> T (in isoform 3, isoform 4 and
FT isoform 6).
FT /FTId=VSP_000568.
FT VARSPLIC 824 869 Missing (in isoform 2).
FT /FTId=VSP_000569.
FT VARSPLIC 1142 1142 D -> VSKRCDKQPAYAPTTTDHQHPNYPQKY (in
FT isoform 6).
FT /FTId=VSP_000570.
FT CONFLICT 391 391 I -> V (IN REF. 2; AAL50790).
FT CONFLICT 894 894 P -> A (IN REF. 2).
SQ SEQUENCE 1186 AA; 131692 MW; BAE8CDEF240E647A CRC64;

Query Match 4.2%; Score 96.5; DB 1; Length 1186;
Best Local Similarity 18.9%; Pred. No. 15;
Matches 66; Conservative 51; Mismatches 114; Indels 119; Gaps 16;

Qy 133 EFCHSDFEDASQGS DTRICPPSSLLPADRKW----GFITVGYRGSC TLGREGQADAKF-- 186
| | : | | | | | | | : : | | | |
Db 253 EVCPECYLAACQKRDNWFCEPCS-NPHPLVWAKLKGF--PFWPAKALRD KDGQVDARFFG 309
Qy 187 -----RRVPRILVCGRISLAKEVFGETLNE-----SRDP 215
: : | : | : | : |

Db	310 QHDRAWVPINNCYLMSKEIP-----FSVKKTKSIFNSAMQEMEVYVENIRRKFGVFNYS	364
Qy	216 DRAPERYTSRFYL-----KFKHLERAFDM-----	239
	: : : :	
Db	365 FRTPYTPNSQYQMLLDPTNPSAGTAKIDKQEKVKLNFDMTASPKILMSKPVLSGGTGRR	424
Qy	240 -LSECGFHMVACNSSV-TASFINQYTDDKIWSSY----TEYVFYREPSRWSPSHCDCCCK	293
	: : : : : : : :	
Db	425 SLSDMPRSPMSTNSSVHTGSDVEQDAEKKATSSHFSASEESMDFLDKSTASPA-----	477
Qy	294 NGKGDKEGESGTSCNDLSTSSCDSQSEASSPQETVICGPVTRQTNIQTLDRPIKKGPVQL	353
	: : : : : : :	
Db	478 ---STKTGQAG-----SLSGSPKPFSPQ---LSAPITTKT-----DKTSTTGSILN	517
Qy	354 IQQSEMRRKSDLLRILTSGSRESN---MSSKKKAVKEK--LSIEEELEKC	398
	: : : : : : : : : : : : :	
Db	518 LNLDRSKAEMDLKELSESVOQQSTPVPLISPKRQIRSRFQLNLDKTIESC	567

Search completed: January 29, 2004, 02:54:05
Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 29, 2004, 02:30:11 ; Search time 64 Seconds
(without alignments)
1725.727 Million cell updates/sec

Title: US-10-056-884A-2
Perfect score: 2284
Sequence: 1 MALSGNCSRYYPREQGSAVP.....DRFPERKHPWQSELLRKYHL 428

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Match Length	DB	ID		Description

1	2271	99.4	435	4	Q9P2M9	Q9p2m9	homo	sapien
2	1278.5	56.0	476	11	Q8C906	Q8c906	mus	musculu
3	1272	55.7	477	11	Q8C9B0	Q8c9b0	mus	musculu
4	1260.5	55.2	476	11	Q8BR74	Q8br74	mus	musculu
5	1125.5	49.3	438	11	Q8CAA9	Q8caa9	mus	musculu
6	921.5	40.3	346	11	Q8C4C2	Q8c4c2	mus	musculu
7	888.5	38.9	292	11	Q8C7J6	Q8c7j6	mus	musculu
8	832	36.4	325	4	Q96CX2	Q96cx2	homo	sapien
9	538.5	23.6	228	5	Q9VDH3	Q9vdh3	drosophila	
10	537	23.5	111	11	Q9CQU2	Q9cqu2	mus	musculu
11	389.5	17.1	156	11	Q8CBQ4	Q8cbq4	mus	musculu
12	208.5	9.1	283	11	Q8K0E1	Q8k0e1	mus	musculu
13	204	8.9	216	4	Q8N3Q9	Q8n3q9	homo	sapien
14	204	8.9	229	4	Q8IU75	Q8iu75	homo	sapien
15	204	8.9	272	4	Q8N5I3	Q8n5i3	homo	sapien
16	202.5	8.9	228	4	Q8TCA6	Q8tca6	homo	sapien
17	202.5	8.9	237	4	Q8NBS6	Q8nbs6	homo	sapien
18	201.5	8.8	237	11	Q8BNL5	Q8bnl5	mus	musculu
19	201.5	8.8	283	4	Q96SI1	Q96sil	homo	sapien
20	196	8.6	191	11	Q8C6V1	Q8c6v1	mus	musculu
21	194	8.5	259	11	Q9CYK4	Q9cyk4	mus	musculu
22	193.5	8.5	237	4	Q8NC69	Q8nc69	homo	sapien
23	192	8.4	259	11	Q9D7X1	Q9d7x1	mus	musculu
24	192	8.4	259	11	Q8CCQ3	Q8ccq3	mus	musculu
25	189	8.3	225	4	Q9BQ13	Q9bql3	homo	sapien
26	189	8.3	259	4	Q8WVF5	Q8wvf5	homo	sapien
27	187	8.2	333	4	Q8WUN2	Q8wun2	homo	sapien
28	169.5	7.4	207	5	O16612	O16612	caenorhabdi	
29	168.5	7.4	234	4	Q9BVI6	Q9bvi6	homo	sapien
30	167.5	7.3	338	5	Q9W2F9	Q9w2f9	drosophila	
31	166	7.3	234	4	Q96N73	Q96n73	homo	sapien
32	165	7.2	222	11	Q8C004	Q8c004	mus	musculu
33	165	7.2	234	11	Q8R3T6	Q8r3t6	mus	musculu
34	163.5	7.2	288	4	Q8IVR0	Q8ivr0	homo	sapien
35	163.5	7.2	289	4	Q96MP8	Q96mp8	homo	sapien
36	163	7.1	234	4	Q9NXV2	Q9nxv2	homo	sapien
37	161.5	7.1	239	11	Q8C0S7	Q8c0s7	mus	musculu
38	161.5	7.1	289	11	Q8BJK1	Q8bjk1	mus	musculu
39	159	7.0	234	11	Q8VC57	Q8vc57	mus	musculu
40	158.5	6.9	272	5	Q18776	Q18776	caenorhabdi	
41	158	6.9	670	5	O17001	O17001	caenorhabdi	
42	157.5	6.9	211	5	Q9W579	Q9w579	drosophila	
43	157.5	6.9	308	5	O76889	O76889	drosophila	
44	156	6.8	220	5	Q18986	Q18986	caenorhabdi	
45	153	6.7	298	10	Q9SE95	Q9se95	arabidopsis	

ALIGNMENTS

RESULT 1

Q9P2M9

ID Q9P2M9 PRELIMINARY; PRT; 435 AA.
AC Q9P2M9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE Hypothetical protein KIAA1317 (Fragment).
 GN KIAA1317.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=20181126; PubMed=10718198;
 RA Nagase T., Kikuno R., Ishikawa K., Hirose M., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes.XVI.
 RT The complete sequences of 150 new cDNA clones from brain which code
 RT for large proteins in vitro.";
 RL DNA Res. 7:65-73(2000).
 DR EMBL; AB037738; BAA92555.1; -.
 DR InterPro; IPR000210; BTB_POZ.
 DR InterPro; IPR003131; K_tetra.
 DR Pfam; PF02214; K_tetra; 1.
 DR SMART; SM00225; BTB; 1.
 KW Hypothetical protein.
 FT NON_TER 1 1
 SQ SEQUENCE 435 AA; 49936 MW; 5437FD0FED211B6B CRC64;

Query Match 99.4%; Score 2271; DB 4; Length 435;
 Best Local Similarity 99.5%; Pred. No. 5e-198;
 Matches 426; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	MALSGNCSRYYPREQGSAVPNSFPEVVVELNVGGQVYFTRHSTLISIPHSLLWKMFSKRD	60
Db	8	MALSGNCSRYYPREQGSAVPNSFPEVVVELNVGGQVYFTRHSTLISIPHSLLWKMFSKRD	67
Qy	61	TANDLAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLDPHFPEKGRLKREAEYFQLPDLVK	120
Db	68	TANDLAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLDPHFPEKGRLKREAEYFQLPDLVK	127
Qy	121	LLTPDEIKQSPDEFCHSDFEDASQGS DTRICPPSSLLPADRKWGFITVGYRG SCTLGREG	180
Db	128	LLTPDEIKQSPDEFCHSDFEDASQGS DTRICPPSSLLPADRKWGFITVGYRG SCTLGREG	187
Qy	181	QADAKFRRVPRI LVCGRISLAKEVFGETL NESRDPDRAPER YTSRFY LKFKHLERAFDML	240
Db	188	QADAKFRRVPRI LVCGRISLAKEVFGETL NESRDPDRAPER YTSRFY LKFKHLERAFDML	247
Qy	241	SECGFHMVACN SSVTASFINQYTD DDKIWSSYTEYVFYREPSRWSPSHCDCCCKNGKGDKE	300
Db	248	SECGFHMVACN SSVTASFINQYTD DDKIWSSYTEYVFYREPSRWSPSHCDCCCKNGKGDKE	307
Qy	301	GESGTSCNDLSTSSCDSQSEASSPQETVICGPVTRQTNIQTLD RPIKKG PVQLIQQSEMR	360
Db	308	GESGTSCNDLSTSSCDSQSEASSPQETVICGPVTRQTNIQTLD RPIKKG PVQLIQQSEMR	367
Qy	361	RKSDLLRILTSGSRESNMSSKKKAVKEKLSIEEELEKCIQDFLKKKIPDRFPERKHPWQS	420
Db	368	RKSDLLRILTSGSRESNMSSKKKAVKEKLSIEEELEKCIQDFLKKKIPDRFPERKHPWQS	427
Qy	421	ELLRKYHL	428

Db 428 ||||| 435
 ELLRKYHL

RESULT 2

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ID      Q8C906                PRELIMINARY;          PRT;      476 AA.
AC      Q8C906;
DT      01-MAR-2003 (TrEMBLrel. 23, Created)
DT      01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT      01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE      Hypothetical protein.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX      MEDLINE=22354683; PubMed=12466851;
RA      The FANTOM Consortium,
RA      the RIKEN Genome Exploration Research Group Phase I & II Team;
RT      "Analysis of the mouse transcriptome based on functional annotation of
RT      60,770 full-length cDNAs.";
RL      Nature 420:563-573(2002).
DR      EMBL; AK043351; BAC31527.1; -.
KW      Hypothetical protein.
SQ      SEQUENCE      476 AA;  52782 MW;  219BEC5D104A53DF CRC64;

```

Qy	16	GSAVPNSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSKRDTA-----NDLAKDSK	70
Db	35	: : : : : :	
Qy	71	GRFFIDRDGFLFRYILDYLRDRQVVLDPHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQS	130
Db	95	: : : : : : :	
Qy	131	P--DEFCHSDFED-ASQGS DTRICPPSSLLPA-----DRKWGFITV	168
Db	155	: : : : :	
Qy	169	GYRGSCTLGREGQADAKFRRVPRILVCGRISLAKEVFGETL NESRDPDRAPER YTSRFYL	228
Db	215	: : : : :	
Qy	229	KFKHLERAFDMLSECGFHMVACNSSVTASFINQYTDDKIWSSYTEYVFYREPSR-WSPSH	287
Db	275	: : : : : : :	
Qy	288	CDCCCKNGK-GDKEGESGTSCNDLSTSSCDSQSEASSPQETVICGP-----VTRQTNIQ	340
Db	335	: : :	
Qy	35	GPCAPSPFPEVVELNVGGQVYVTKHSTLLSVPDSTLASMFSPSSPRGGARRRGDLPRDSR	94
Qy	71	ARFFIDRDGFLFRYVLDYLRDKQLALPEHFPEKERLLREAEFFQLTDLVKLLSPKVTKQN	154
Qy	131	SLNDECCQSDLEDNVSQGS DALLLRGAAAGAPSGSGAHGVSGVVGGSAPDKRSGFLT	214
Qy	169	GYRGSYTTVRDNQADAKFRRVARIMVCGRIALAKEVFGDTL NESRDPDRQPEKYTSRFYL	274
Qy	229	KFTYLEQAFDRLSEAGFHMVACNSSSGTAAAFVNQYRDDKIWSSYTEYIFFRPPQKIVSPKQ	334
Qy	288	EHEDRKRDKVTDKGS EGTSCNELSTSSCDSHSEASTPOD----NPANTQAAAAHQPN	390

Qy 341 TLDRIKKGPVQLIQQSEMRRKSDLRLITSGSRESNMSSKKKAVKEKLSIEEELEKCIQ 400
 ||||| :| ||| : : |||||:| : | | |||:|:| || | ||||:||||:||||
 Db 391 TLDRPSRKAPVQWMPPDPKRRKSELFQSLISKSRETNLSKKK--VCEKLSVEEEMKKCIQ 448

Qy 401 DFLKKKIPDRFPERKHPWQSELLRKYHL 428
 || | ||| ||||| |||||:| | |
 Db 449 DFKKIHIPDCFPERKRQWQSELLQKYGL 476

RESULT 3

Q8C9B0

ID Q8C9B0 PRELIMINARY; PRT; 477 AA.
 AC Q8C9B0;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AK042569; BAC31296.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 477 AA; 52978 MW; EB44F32A68E9AEA4 CRC64;

Query Match 55.7%; Score 1272; DB 11; Length 477;
 Best Local Similarity 59.7%; Pred. No. 4.4e-107;
 Matches 268; Conservative 46; Mismatches 93; Indels 42; Gaps 10;

Qy 16 GSAVPNSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSKP--RDTA----NDLAKDS 69
 | | : |||:||||||| | :|||:|:| | | ||| | | || :||
 Db 35 GPCAPSPFPEIVELNVGGQVYVTKHSTLLSVPDSTLASMFSPPSRGRAPRRRGDLPRDS 94

Qy 70 KGRFFIDRDGFLFRYILDYLRDRQVVLDPHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQ 129
 : ||||| |||||:|||||:| : ||||| || ||||:||| |||||:| ||
 Db 95 RARFFIDRDGFLFRYVLDYLRDKQLALPEHFPEKERLLREAEFFQLTDLVKLLSPKVTKQ 154

Qy 130 SP--DEFCHSDFED-ASQGS DTRICPPSSLLPA-----DRKWGFIT 167
 : || | || | ||| : : | | : ||:|
 Db 155 NSLNDECCQSDLEDNVSQGS DALLLRGAAAGAPSGSGAHGVSGVVGGSAPDKRSGFLT 214

Qy 168 VGYRG SCTLGREGQADAKFRRVPRIILVCGRISLAKEVFGETL NESRDPDRAPER YTSRFY 227
 :|||| | | : ||||| |||:||||:|||||:||||| |||:|||||
 Db 215 LGYRG SYTTVRDNQADAKFRRVARIMVCGRIALAKEVFGDTL NESRDPDRQPEKYTSRFY 274

Qy 228 LKFKHLERAFDMLSECGFHMVACNSSVTASFINQYTDDKIWSSYTEYVFYREPSR-WSPS 286
 ||| :||:| | || ||||| |||:|:| ||||| |||:| | : ||
 Db 275 LKFTYLEQAFDRLSEAGFHMVACNSSGTA AFVNQYRDDKIWSSYTEYIFFRPPQKIVSPK 334

Qy 287 HCDCCCKNGK-GDKEGESGTSCNDLSTSSCDSQSEASSPQETVICGP-----VTRQTNI 339
 | | || |||||:||||||| |||:|: | |
 Db 335 QEHEDRKRDKVTDKGSESGTSCNELSTSSCDSHSEASTPQD----NPANTQQAAAHQPNT 390
 Qy 340 QTLDRIKKGPVQLIQQSEMRRKSDLLRIITSGSRESNMSSKKKAVKEKLSIEEELEKCI 399
 |||| :| ||| : : || |:| : | |||:|: || | |||:||||:|
 Db 391 LTLDPRSRKAPVQWMPDPKRRNSELFQSLISKSRETNLSKKK--VCEKLSVEEEMKKCI 448
 Qy 400 QDFLKKKIPDRFPERKHPWQSELLRKYHL 428
 || | ||| ||||| |||||:| |
 Db 449 QDFKKIHIPDCFPERKRQWQSELLQKYGL 477

RESULT 4

Q8BR74

ID Q8BR74 PRELIMINARY; PRT; 476 AA.
 AC Q8BR74;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AK045439; BAC32368.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 476 AA; 52892 MW; 381C955B9A3DE3F1 CRC64;

Query Match 55.2%; Score 1260.5; DB 11; Length 476;
 Best Local Similarity 59.2%; Pred. No. 4.9e-106;
 Matches 265; Conservative 45; Mismatches 97; Indels 41; Gaps 9;

Qy 16 GSAVPNSFPEVVVELNVGGQVYFTRHSTLISIPHSLLWKMFSKRDTA-----NDLAKDSK 70
 | |: ||||| ||||| |:|||:|:| | | ||| | :|:
 Db 35 GPCAPSPFPEVVVELNVGGQVYVKHSTLLSVDPSTLASMFSPPSGGARRRGDLPRDSR 94
 Qy 71 GRFFIDRDGFLFRYILDYLRDRQVVLDPHFPEKGRLKREAEYFQLPDIVKLLTPDEIKQS 130
 ||||| |||||:|||||:|: ||:|||| || ||||:| |||||:| ||:
 Db 95 ARFFIDRDGFLFRYVLDYLRDKQLALPEHFPEKERLLREAEFFQLTDLVKLLSPKVTKQN 154
 Qy 131 P--DEFCHSDFED-ASQGS DTRICPPSSLLPAD-----RKWGFITV 168
 || | || || ||| : : | :|:|:
 Db 155 SLNDECCQSDLEDNVSQGSSDALLLRGAAAGAPSGSGAHGVSGVVGGSAPYKRSGLTL 214
 Qy 169 GYRGSTLGREGQADAKFRRVPRILVCGRISLAKEVFGETLNESRDPDRAPERYSRFYL 228
 |||| | |: ||||| ||:||||:|||||:||||| ||:|||||

Db 215 GYRGSYTTVRDNQADAKFRRVARIMVCGRIALAKEVFGDTLINESRDPDRQPEKYTSRFYL 274

Qy 229 KFKHLERAFDMLSECGFHMVACNSSVTASFINQYTDKDWSSYTEYVFYREPSR-WSPSH 287
 || :||:|||| ||| ||||| ||||| |||:|:|||| ||||| |||||:|:| | : ||

Db 275 KFTYLEQAFDRLSEAGFHMVACNSSGTAAAFVNQYRDDKIWSSYTEYIFFRPPQKIVSPKQ 334

Qy 288 CDCCKNGK-GDKEGESGTSCNDLSTSSCDSQSEASSPQETVICGP-----VTRQTNIQ 340
 | | || |||||:| ||||| ||||:|: | | |

Db 335 EHEDRKRDKVTDKGSESGTSCNELYTSSCDSHSEASTPQD----NPANTQQAAAHQPNTL 390

Qy 341 TLDRIPIKGPVQLIQQSEMRRKSDLLRILTSGSRESNMSSKKKAVKEKLSIEEELEKCIQ 400
 ||||| :| ||| : : || |:| : | | |||:|:| || | ||||:||||:||||

Db 391 TLDRPSRKAPVQWMPDPKRRNSELFQSLISKSRETNLSKKK--VCEKLSVEEEMKKCIQ 448

Qy 401 DFLKKKIPDRFPERKHPWQSELLRKYHL 428
 || | ||| |||| | ||||:| | |

Db 449 DFKKIHIPDCFFPERKRQWQSELLQKYGL 476

RESULT 5

Q8CAA9

ID Q8CAA9 PRELIMINARY; PRT; 438 AA.

AC Q8CAA9;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Hypothetical protein (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;

RX MEDLINE=22354683; PubMed=12466851;

RA The FANTOM Consortium,

RA the RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

DR EMBL; AK039167; BAC30262.1; -.

KW Hypothetical protein.

FT NON_TER 438 438

SQ SEQUENCE 438 AA; 48062 MW; 7499764AE3745B1D CRC64;

Query Match 49.3%; Score 1125.5; DB 11; Length 438;
 Best Local Similarity 58.3%; Pred. No. 8.4e-94;
 Matches 239; Conservative 42; Mismatches 88; Indels 41; Gaps 9;

Qy 16 GSAVPNSFPEVVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPPKRDTA-----NDLAKDSK 70
 | |: ||||| ||||| |:|:|:| | | |||| | | :|:

Db 35 GPCAPSPFPEVVVELNVGGQVYVTKHSTLLSVPDSTLASMFSPPSPRGARRRGDLPRDSR 94

Qy 71 GRFFIDRDGFLFRYILDYLRDQVVLDPHFPEKGRLLKREAEYFQLPDLVKLLTPDEIKQS 130
 ||||| |||||:|||||:|: |:|:| | | ||||:| | |||||:| | |:

Db 95 ARFFIDRDGFLFRYVLDYLRDQQLALPEHFPEKERLLREAEFFQLTDLVKLLSPKVTKQN 154

Qy 131 P---DEFCHSDFED-ASQGS DTRICPPSSLLPA-----DRKWGFITV 168
 | : | | | | | | | : : | | : | : | : | :
 Db 155 SLNDKCCQSDLEDNVSQGSSDALLLRGAAAGAPSGSGAHGVSGVVGGSAPDKRSQFLTL 214

Qy 169 GYRG SCTLGREGQADAKFRRVPRILVCGRISLAKEVFGETL NESRDPDRAPERYSRFYL 228
 | | | | | | : | | | | | | | : | | | | : | | | | | | | : | | | | |
 Db 215 GYRG SYTTVRDNQADAKFRRVARIMVCGRIALAKEVF GDTL NESRDPDRQPEKYTSRFYL 274

Qy 229 KFKHLERAFDMLSECGFHMVACNSSVTASFINQYTDDKIWSSYTEYVFYREPSR-WSPSH 287
 | | : | : | | | | | | | | | | | | | | | | | : | | : | |
 Db 275 KFTYLEQAFDRLSEAGFHMVACNSSGTAA FVNQYRDDKIWSSYTEYIFFRPPQKIVSPKQ 334

Qy 288 CDCCCKNGK-GDKEGESGTSCNDLSTSSCDSQSEASSPQETVICGP-----VTRQTNIQ 340
 | | | | | | | | | | | | | | | | | : | | : | | | | |
 Db 335 EHEDRKRDKVTDKGSESGTSCNELSTSSCDSHSEASTPQD----NPANTQQAAAHQPNTL 390

Qy 341 TLD RPIKKGPVQLIQQSEMRRKSDLLRILTSGSRESNMSSKKKAVKEKLS 390
 | | | | | : | | | : : | | | : | | | | : | | | | | | |
 Db 391 TLD RPSRKAPVQWMP PDKRRNSELFQSLISKSRETNLSKKK--VCEKLS 438

RESULT 6

Q8C4C2

ID Q8C4C2 PRELIMINARY; PRT; 346 AA.
 AC Q8C4C2;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 DR EMBL; AK082563; BAC38532.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 346 AA; 37981 MW; 0A52BB7F33D59D37 CRC64;

Query Match 40.3%; Score 921.5; DB 11; Length 346;
 Best Local Similarity 62.5%; Pred. No. 2.2e-75;
 Matches 182; Conservative 32; Mismatches 50; Indels 27; Gaps 4;

Qy 16 GSAVPNSFPEVVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTA-----NDLAKDSK 70
 | | : | | | | | | | | | | | : | | | : | | | | | | | : | | :
 Db 35 GPCAPSPFPEVVVELNVGGQVYVTKHSTLLSVPDSTLASMFSPPRGARRRGDLPRDSR 94

Qy 71 GRFFIDRDGFLFRYILDYLRDRQVLPDHFPEKGR LKREAEYFQLPDLVKLLTPDEIKQS 130
 | | | | | | | | | : | | | | : | : | | | | | | | | | : | : | : | :
 Db 95 ARFFIDRDGFLFRYVLDYLRDQLALPEHFPEKERLLREAEFFQLTDLVKLLSPEVTKQN 154

Qy	131	P--DEFCHSDFED-ASQGS DTRICPPSSLLPA-----DRKWGFITV	168
		: : : : : :	
Db	155	SLNDECCQSDLEDNVSQGS DALLRGAAAGAPSGSGAHGVSGVVGGGSAPDKRSGFLTL	214
Qy	169	GYRGSCTLGREGQADAKFRRVPRI LVCGRIS LAKEVFGETL NESRDPDRAPER YTSRFYL	228
		: : : : :	
Db	215	GYRGSYTTVRDNQADAKFRRVARIMVCGRIALAKEVFGDTL NESRDPDRQPEKYTSRFYL	274
Qy	229	KFKHLERAFDMLSECGFHMVACNSSVTASFINQYTD DDKIWSSYTEYVFYRE	279
		: : : : :	
Db	275	KFTYLEQAFDRLSEAGFHMVACNSSGTA AFVNQYRDDKIWSSYTEYIFFRK	325

Q8C7J6

```

ID Q8C7J6 PRELIMINARY; PRT; 292 AA.
AC Q8C7J6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical K+ channel tetramerisation domain containing
DE protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK050097; BAC34065.1; -.
KW Hypothetical protein.
SQ SEQUENCE 292 AA; 33285 MW; 4986B75B7C054D44 CRC64;

```

Qy	1	MALSGNCSRYYPREQGSAVPNSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRD	60
		: : :: : :	
Db	1	MAMPEKSSDVKPTEE----CGSFPEIIELVGGQVYITRYPTLISIPGSRLWEMFSVKNP	56
Qy	61	TANDLAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLDPDHFPEKGRLKREAEIFQLPDLVK	120
		: : : : : : :	
Db	57	CS--LIQDNKGRFFIDRDGFLFRYVLDYMRDMQVVLDPDHFPECGRLHREAEIFKLPELAK	114
Qy	121	LLTP--DEIKQSPDEFCHSDFDASQGSDT-----RICPPSSLL	157
		: ::: :: :	
Db	115	MLAPKMKNLSIGNDSCPIDLEELSPSIDTTFNFSSTNSIHISGPDNPMVLRAAPGSEL-	173
Qy	158	PADRWGFIITVGYRGSCITLGREGQADAKFRRVPRILVCGRISLAKEVFGETLNESRDPDR	217

```

          :| ||||:|||| | |||: ||||| ||: |||: ||||| ||: |||||
Db      174 ---KKAGFITIGYRGSYTLGRDSQADAKFRRVARIMVCGKISLAKEVFGDTLNESRDPDR 230
Qy      218 APERYTSRFYLFKFKHLERAFDMLSECGFHMVACNSSVTASFINQYTDDKIWSSYTEYVFY 277
          |||||: ||| | ||: ||| |:: ||||| ||: | : : |||: ||: |||||
Db      231 PPERYTSRYLKFETFLAQAFDKLADAGFHMVACNSTGTCTVTHDQTDRIWTSYTEYVFY 290
Qy      278 RE 279
          ||
Db      291 RE 292

```

RESULT 8

Q96CX2

```

ID   Q96CX2          PRELIMINARY;          PRT;    325 AA.
AC   Q96CX2;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis, and Embryonic carcinoma;
RA   Strausberg R.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC013764; AAH13764.1; -.
DR   InterPro; IPR000210; BTB_POZ.
DR   InterPro; IPR003131; K_tetra.
DR   Pfam; PF02214; K_tetra; 1.
DR   SMART; SM00225; BTB; 1.
KW   Hypothetical protein.
SQ   SEQUENCE    325 AA;  35700 MW;  6254CC18E27275A9 CRC64;

```

```

Query Match          36.4%; Score 832; DB 4; Length 325;
Best Local Similarity 54.0%; Pred. No. 2.8e-67;
Matches 170; Conservative 41; Mismatches 56; Indels 48; Gaps 6;

```

```

Qy      4 SGNCSRYYPREQGSAVPNSFPEVVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTAN 63
          ||: |      || | ||::||| || || ||: ||: ||||: ||: ::
Db      20 SGSSS-----SSAEPPLFPDIVELNVGGQVYVTRRCTVVSVPDSSLWRMFTQQQ--PQ 70
Qy      64 DLAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLDPDHFPEKGRLLKREAEIFQLPDLVKLL- 122
          :||: |||||: ||||| ||||| ||: ||||: ||: ||: |||||: ||: ||: |
Db      71 ELARDSKGRFFLDRDGFLFRYILDYLRDLQLVLPDYFPERSRLQREAEIFELPELVRLG 130
Qy      123 TPDEIKQSP-----DEFCHSDFEDASQ-----GS 146
          | : |      || : : |      |:
Db      131 APQQPGPGPPPSRRGVHKEGSLGDELLPLGYSEPEQQEGASAGAPSPTLELASRSPSGGA 190
Qy      147 DTRICPPSSLLPADRWGFITVGYRGSCTLGREGQADAKFRRVPRILVCGRISLAKEVFG 206
          : || | | : ||: |||| |:: ||||| || |||: |||||
Db      191 AGPLLTQSLSLDGSRRSYITIGYRGSYTIGRDAQADAKFRRVARITVCGKTSLAKEVFG 250

```

Qy 207 ETLNESRDPDRAPERYTSRFYLKFKHLERAFDMLSECGFHMVACNSSVTASFIN--QYTD 264
 :|||||:|||||:||||| ||:|||| ||| |||||:|: | :| : :
 Db 251 DTLNESRDPDRPPERYSRYYLKFNLFLEQAFDKLSESGFHMVACSSSTGTCAFASSTDQSE 310

Qy 265 DKIWSSYTEYVFYRE 279
 ||||:||||| ||
 Db 311 DKIWTSYTEYVFCRE 325

RESULT 9

Q9VDH3

ID Q9VDH3 PRELIMINARY; PRT; 228 AA.
 AC Q9VDH3;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE CG10830 protein (GH08630P).
 GN CG10830.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003732; AAF55820.1; -.
 DR EMBL; AY060259; AAL25298.1; -.
 DR FlyBase; FBgn0038839; CG10830.
 DR InterPro; IPR000210; BTB_POZ.
 DR InterPro; IPR003131; K_tetra.
 DR Pfam; PF02214; K_tetra; 1.
 DR SMART; SM00225; BTB; 1.
 SQ SEQUENCE 228 AA; 25970 MW; 001CB30B990EB6A1 CRC64;

Query Match 23.6%; Score 538.5; DB 5; Length 228;
 Best Local Similarity 44.3%; Pred. No. 9e-41;
 Matches 116; Conservative 44; Mismatches 61; Indels 41; Gaps 7;

QY 24 PEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSKRDRTANDLAKDSKGRFFIDRDGFLFR 83
 ||::||||| | | :||: :|| ::| ||: |||||:|:|||| ||
 Db 2 PEIIEINVGGVSYTTLATLLQDKSTLLAELFGEGRDS---LAKDSKGRYFLDRDGVLF 58

 QY 84 YILDYLRDRQVVLDPHFPEKGRLEAEYFQLPDLVKLLTPDEIKQSPDEFCHSDFEDAS 143
 |||:|:|: : ||: | |: || |||:|:| : : : :
 Db 59 YILDFLRDKALHLPEGFREQRLLREAEHFKLTMALCECIRSER----- 101

 QY 144 QGSDTRICPPSSLLPADRKWGFITVGYRGSCITLGREGQADAKFRRVPRILVCGRISLAKE 203
 | | || | ||:|||| |::| || |||:| |||||:: :|
 Db 102 ---DAR--PP-----GCITIGYRGSFQFGKDLADVKFRKLSRILVCGRVAQCRE 146

 QY 204 VFGETLINESRDPDR-APERYTSRFLKFKHLERAFDMLSECGFHMV-ACNSSVTASFINQ 261
 |||:||||||| :|||:|:| :|:| | : | : |
 Db 147 VFGDTLINESRDPDHGGTDRYTSRFLKHCYIEQAFDNLHDHGYRMAGSCGSGTAGSAAEP 206

 QY 262 Y----TDDKIWSSYTEYVFYRE 279
 |:: |: | |:| |:
 Db 207 KPGVDTEENRWNHYNEFVFIRD 228

RESULT 10

Q9CQU2

ID Q9CQU2 PRELIMINARY; PRT; 111 AA.

AC Q9CQU2;

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)


```
DE   Inferred: KIAA1317 protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK035535; BAC29094.1; -.
SQ   SEQUENCE   156 AA;  17139 MW;  7A94B22AD58D2A3A CRC64;
```

Query Match 17.1%; Score 389.5; DB 11; Length 156;
Best Local Similarity 63.0%; Pred. No. 2e-27;
Matches 75; Conservative 20; Mismatches 15; Indels 9; Gaps 2;

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Qy      4  SGNCSRYYPREQGSAPVNSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRD TAN 63
      ||: |          || |  ||::||||||| ||  |:::| |||:|: ::
Db      20  SGSSS-----SSAEPPLFPDIVELNVGGQVYVTRRCTVVSVPDSLWRFMFTQQQ--PQ 70

Qy      64  DLAKDSKGRFFIDRDGFLFRYILDYLRDRQVLPDHFPEKGRLKREAEYFQLPDLVKLL 122
      :||:|||||:||||||| ||| |::|||:|: ||:|||||:|:|: |
Db      71  ELARDSKGRFFLDRDGFLFRYILDYLRDLQVLPDYFPERSRLOREAEYFELPELVRR 129

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RESULT 12

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Q8K0E1
ID   Q8K0E1                PRELIMINARY;          PRT;    283 AA.
AC   Q8K0E1;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein (Hypothetical BTB/POZ domain containing
DE   protein).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Retina;
RA   Strausberg R.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Embryo;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).

```


DR EMBL; BC031749; AAH31749.1; -.
 DR EMBL; AK034731; BAC28810.1; -.
 DR InterPro; IPR000210; BTB_POZ.
 DR InterPro; IPR003131; K_tetra.
 DR Pfam; PF02214; K_tetra; 1.
 DR SMART; SM00225; BTB; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 283 AA; 31886 MW; 7D67029CD51B8E2B CRC64;

Query Match 9.1%; Score 208.5; DB 11; Length 283;
 Best Local Similarity 26.0%; Pred. No. 1.3e-10;
 Matches 74; Conservative 42; Mismatches 100; Indels 69; Gaps 10;

Qy 15 QGSAPNSFPEV---VELNVGGQVYFTRHSTLISIPHSLLWKMFSKPRDITANDLAKDSKG 71
 || :| : | :||| :| : :|| | | : :| : | |
 Db 43 QGIPLPAQLTKANAPVHIDVGGHMYTSSLATLTYPDSRISRLFNTEPIVLDLQKQ--- 99
 Qy 72 RFFIDRDGFLFRYILDYLRDRQVVLDPHFPEKGRKREAEYFQLPDLVKLLTPDEIKQSP 131
 :||||| :||||| :|| :||| | : | | | :| : | :
 Db 100 HYFIDRDGEIFRYILSFLRTSKLLLPDDFKDFNLLYEEARYYQLQPMVRELERWQ----- 154
 Qy 132 DEFCHSDFEDASQGS DTRICPPSSLLPADRKWGFITVGYRGSCITLGREGQADAKFRRVPR 191
 :| | :| | : | : || | |
 Db 155 -----QDQEQRRRSRACD-----CLVVRVTPDLGE-----R 180
 Qy 192 ILVCGRISLAKEVFGET-----LNESRDPDRAPERYTSRFYLFKFKHLERAFDMLSE 242
 | : | :| :||| || :|| | : | : :| : | :
 Db 181 IALSGEKALIEEVFPETGDVMCNSVNAGWNQDPHTV-IRFPLNGYCRLNSVQ-VLERLFQ 238
 Qy 243 CGFHMVA-CNSSVTASFINQYTDDKIWSSYTEYVFYREPSRWSPS 286
 || :| | | : | :||| || | | :
 Db 239 RGFSVAASC GGGVDS-----SQFSEYVLCREERRPQPT 271

RESULT 13

Q8N3Q9

ID Q8N3Q9 PRELIMINARY; PRT; 216 AA.
 AC Q8N3Q9;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN DKFZP313I0334.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ansorge W., Wirkner U., Mewes H.W., Weil B., Wiemann S.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AL832695; CAD38633.1; -.
 DR InterPro; IPR000210; BTB_POZ.
 DR InterPro; IPR003131; K_tetra.
 DR Pfam; PF02214; K_tetra; 1.
 DR SMART; SM00225; BTB; 1.
 KW Hypothetical protein.

FT	NON_TER	1	1	
SO	SEQUENCE	216 AA;	24790 MW;	1C6DC5158A3F1B2C CRC64;

```

Qy      22 SFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDANDLAKDSKGRFFIDRDGFL 81
      | :| ||||:: || |:  | | :|  | :  | :| ||| |
Db      5 SSQELVTNLVGGKIFTTRFSTIKQFPASRLARML---DGRDQEFKMVGQIFVDRDGDL 60

Qy      82 FRYILDYLRDRQVVLDPDHFEKGRCLKREAEYFQLPDLVKLLTPDEIKQSP 131
      | :|||:| |::|| | : ||:| | ::| || || | : : |
Db      61 FSFILDFLRTHOLLLPTEFSDYLRLOREALFYELRSIVDLLNPYLLQPRP 110

```

Query Match 8.9%; Score 204; DB 4; Length 229;
Best Local Similarity 42.7%; Pred. No. 2.4e-10;
Matches 47; Conservative 20; Mismatches 39; Indels 4; Gaps 1;

```

Qy      22 SFPEVVELNVGGQVYFTRHSTLISIPHSLWKMFSPKRDANDLAKDSKGRFFIDRDGFL 81
      | |:| ||||:: || |: | | :| | : | |:| ||| |
Db      2 SSQELVTLNVGGKIFTTRFSTIKQFPASRLARML----DGRDQEFKMGVGGQIFVDRDGDL 57

Qy      82 FRYILDYLRDRQVVLDPHFPEKGRLKREAEYQLPDLVKLLTPDEIKQSP 131
      | :|||:| |::| | : |::|||:::| || | : |
Db      58 FSEILDFLRTHOLLLPTEFSDYLRLOREALFYELRSIVDLLNPYILLOPRP 107

```

RESULT 15

Q8N5I3

ID Q8N5I3 PRELIMINARY; PRT; 272 AA.
 AC Q8N5I3;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein BC013764 (Putative regulator of potassium
 DE channels protein variant 2) (Putative potassium channel proteins
 DE regulator protein variant B).
 GN KCNRG.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Tyazhelova T.V., Ivanov D.V., Guskova A.A., Panchin Y.V.,
 RA Baranova A.V.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Tyazhelova T.V., Ivanov D.V., Baranova A.V.;
 RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC032343; AAH32343.1; -.
 DR EMBL; AY129654; AAN06091.1; -.
 DR EMBL; AY169388; AAO11778.1; -.
 DR InterPro; IPR000210; BTB_POZ.
 DR InterPro; IPR003131; K_tetra.
 DR Pfam; PF02214; K_tetra; 1.
 DR SMART; SM00225; BTB; 1.
 KW Hypothetical protein; Ionic channel.
 SQ SEQUENCE 272 AA; 31047 MW; 5018F55980F0BBA5 CRC64;

Query Match 8.9%; Score 204; DB 4; Length 272;
 Best Local Similarity 42.7%; Pred. No. 3.1e-10;
 Matches 47; Conservative 20; Mismatches 39; Indels 4; Gaps 1;

QY 22 SFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFL 81
 | |:| |||||::: || ||: | | | : | : | |:| |||| |
 Db 2 SSQELVTLNVGGKIFTTRFSTIKQFPASRLARML----DGRDQEFKMGVGGQIFVDRDGDL 57
 QY 82 FRYILDYLRDRQVVLDPDFPEKGRLLKREA EYFQLPDLVKLLTPDEIKQSP 131
 | :|||:| |::|| | : ||:| | ::| || || | :: |
 Db 58 FSFILDFLRTHQLLLPTEFS DYLRQLREALFYELRSLVDLLNPYLLQPRP 107

Search completed: January 29, 2004, 02:55:16
 Job time : 69 secs